Table III

Gene Name	Coriell DNA Panel(s)	Amplicon No.	Total SNPs	Missense	Silent	UTR	Intronic
Aminopeptidase P (XPNPEP2)	24 + 47 (55AA) +12pt	24	30	0	2	7	21
Bradykinin B1 receptor (BDKRB1)	24+ 95 (8AA, 103 CAU) +12pt	7	14	2	5	3	4
Bradykinin B2 receptor (BDKRB2)	24 (8AA) +12pt	12	36	3	2	14	17
NK1 tachykinin receptor (TACR1)	24 (8AA) +12pt	7	9	0	3	3	3
C1 esterase inhibitor (C1NH)	24 (8AA) +12pt	10	6	2	2	0	2
Kallikrein 1 (KLK1)	7 (7AA) +12pt	5	6	1	1	2	2
Protease Inhibitor 4 (PI4)	7 (7AA) +12pt	8	12	1	3	1	7
Angiotensin Converting Enzyme 2 (ACE2)	7 (7AA) +12pt	20	9	0	0	0	9
Totals:			122	9	18	30	65

Table IV (1 of 2)

GENE_DESCRIPTION	HGNC_ID	SNP_ID	CONTIG_NUM	CONTIG_POS	FLANK_SEQ (REF / ALT)	FLANK_SEQ REF (SEQ ID NO:)	FLANK_SEQ ALT (SEQ ID NO:)	REF_SEQ_ID	REF_SEQ_POS	REF_NT	ALT_NT	EXON	MUTATION_TYPE	REVCOMP	REF_CODON	ALT_CODON	CDNA_SEQ_ID	CDNA_SEQ_POS
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s1	1	127	GCTGTCTCC [C/G] GAGCATGTG	37	100	AL023653.1	82896	C	G	Exon20	Silent	0	CCC	CCG	U90724.1	2085
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s2	4	535	AGAACAGTC [T/C] AGTGTTACA	38	101	AL023653.1	60150	C	T	Intron3	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s3	5	224	CTCACCACC [C/T] TCCCCCAAG	39	102	AL023653.1	74483	T	C	Intron15	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s4	5	392	AGGCCTCAG [T/C] CCAAGCTGA	40	103	AL023653.1	74651	C	T	Intron15	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s5	6	432	CGGGCCCCA [G/A] CCCTCACTC	41	104	AL023653.1	54549	T	C	Intron1	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s6	7	258	TAATAAAAG [A/G] GGGGTGGCC	42	105	AL023653.1	76521	C	T	Intron7	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s7	10	461	AAAAGCAGC [G/A] AAACCCTTT	43	106	AL023653.1	65566	C	T	Intron7	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s8	13	273	CACAGGGG [C/T] GTTTTCAGA	44	107	AL023653.1	68286	A	G	Intron10	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s9	13	324	TTTGCCACC [A/G] TTTCGTGGC	45	108	AL023653.1	68236	T	C	Intron10	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s10	14	856	AGCATGCAC [C/G] TGAGTCACC	46	109	AL023653.1	63088	C	G	Intron7	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s11	15	187	AGGT [T/C] CTCCACCA	47	110	AL023653.1	71620	C	T	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s12	15	194	CCTCCA [C/T] CAAGGCC	48	111	AL023653.1	71627	C	T	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s13	15	218	GACCCAGT [G/A] CAGGGTTAG	49	112	AL023653.1	71651	G	A	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s14	8	221	TTTCCCCGG [G/C] CTCTTCCTT	50	113	AL023653.1	54356	G	C	Exon1	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s15	8	243	GCCTTTCCT [A/G] GGCTCGAGC	51	114	AL023653.1	54334	C	T	Exon1	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s16	14	139	AATATTTAA [C/T] GCTGATCTG	52	115	AL023653.1	66924	A	G	Intron8	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s17	22	809	GAAAGGA [A/C] GACATA	53	116	AL023653.1	77205	T	G	Intron17	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s18	22	964	AGGATTGGC [T/G] CTGGCTTTT	54	117	AL023653.1	77052	A	C	Intron17	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s19	26	195	TGGAGGA [C/T] GGGAGGAG	55	118	AL023653.1	75689	G	A	Intron15	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s20	27	306	TGGCTT [A/G] GAGAGGCTG	56	119	AL023653.1	83469	A	G	Intron20	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s21	27	695	GGTCCCAGG [A/C] CCCAGGAAC	57	120	AL023653.1	83858	C	A	Exon21	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s22	28	710	TACCACACC [C/G] TGGGCCCC	58	121	AL023653.1	83926	C	G	Exon21	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s23	28	1369	GCATTCCAG [C/T] TCTTTCACC	59	122	AL023653.1	84585	C	T	Exon21	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s1	6	307	TGTGGGCC [G/A] GCTCTTCA	60	123	U48231.1	2207	G	A	Exon2	Missense	0	CGG	CAG	NM_000710.1	956
Bradykinin Receptor B1	BDKRB1	AE103s2	4	273	ATAAATGT [T/C] GGCAGCACT	61	124	U48231.1	1380	G	A	Exon2	Silent	0	CCG	CCA	NM_000710.1	129
Bradykinin Receptor B1	BDKRB1	AE103s3	7	958	ACAAAGAAT [T/C]' GATAAGAAA	62	125	U48231.1	2355	A	G	Exon3	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s4	1	196	ACGGACTGA [G/A] ACCCTGTCT	63	126	U48231.1	230	C	T	Exon1	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s5	7	240	CAGTGGCCA [T/C] GCCTATAAT	64	127	U48231.1	3072	G	A	Exon3	Non-CDS	0				
Bradykinin Receptor B2	BDKRB2	AE104s1	10	86	GGCTCCCCC [C/G] GCCGCGCCC	65	128	AL355102.2	98426	C	G	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s2	10	87	GCGCCCCCC [A/G] CCGCGCCCA	66	129	AL355102.2	98427	A	G	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s3	10	462	AGGTCATG [T/A] TCCCCCTCT	67	130	AL355102.2	98802	T	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s4	10	542	GGGATGAGG [C/T] CTGGGGTGC	68	131	AL355102.2	98882	C	T	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s5	10	557	GTGCTGCCT [G/A] TGGGGACAG	69	132	AL355102.2	98897	G	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s6	10	717	AGGAC [A/G] CAGCACAGT	70	133	AL355102.2	99056	G	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s7	7	408	GTCCCACAA [C/G] CCCCCTGCT	71	134	AL355102.2	66369	G	C	Intron2	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s8	5	275	GCACAACCA [T/C] CTGTCCCTG	72	135	AL355102.2	62853	A	G	Exon3	Non-CDS	1			NM_000623.1	2002
Bradykinin Receptor B2	BDKRB2	AE104s9	5	390	TGAGGCATC [A/T] TTACGCAG	73	136	AL355102.2	62738	T	A	Exon3	Non-CDS	1			NM_000623.1	2117
Bradykinin Receptor B2	BDKRB2	AE104s10	5	527	AGGTGCTCA [C/T] TGGCTCCCT	74	137	AL355102.2	62601	A	G	Exon3	Non-CDS	1			NM_000623.1	2254
Bradykinin Receptor B2	BDKRB2	AE104s11	6	579	TGAGTCTT [T/G] CACAGGACA	75	138	AL355102.2	61132	T	G	Exon3	Non-CDS	1			NM_000623.1	3604
Bradykinin Receptor B2	BDKRB2	AE104s12	6	585	CTTTCACAG [G/T] ACAGATGT	76	139	AL355102.2	61136	G	T	Exon3	Non-CDS	1			NM_000623.1	3598
Bradykinin Receptor B2	BDKRB2	AE104s13	6	727	AGACCATCA [T/C] GTGCTCTGG	77	140	AL355102.2	61280	C	T	Exon3	Non-CDS	1			NM_000623.1	3456
Bradykinin Receptor B2	BDKRB2	AE104s14	8	482	ACCATTG [T/C] CATTCCT	78	141	AL355102.2	62290	C	T	Exon3	Non-CDS	1			NM_000623.1	2565
Bradykinin Receptor B2	BDKRB2	AE104s16	9	1010	TAAACAAAA [T/C] TTGCCTAG	79	142	AL355102.2	60403	G	A	3' Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s17	9	1072	CCATGCCAG [A/G] AACCTGGGG	80	143	AL355102.2	60341	C	T	3' Flank	Non-CDS	1				
Tachykinin Receptor 1	TACR1	AE106s1	1	614	CAACTTCTT [T/C] CCCATCGCC	81	144	AC007681.3	103665	A	G	Exon1	Silent	1	TTT	TTC	NM_001058.2	543
Tachykinin Receptor 1	TACR1	AE106s2	2	789	CAGGACCCA [T/G] ATGACACAG	82	145	AC007681.3	25759	G	T	Exon2	Silent	1	ATC	ATA	NM_001058.2	672
Tachykinin Receptor 1	TACR1	AE106s3	4	676	TTCTGCCTG [T/G] CCCCTGCT	83	146	AC007400.3	143458	T	G	Intron3	Non-CDS	1				
Tachykinin Receptor 1	TACR1	AE106s4	6	152	GAATGGGCT [T/C] TTGGGAAAA	84	147	AC007400.3	139028	T	C	Exon5	Non-CDS	1				
Tachykinin Receptor 1	TACR1	AE106s5	6	220	TTTGAGTCA [C/A] ACAGCATGA	85	148	AC007400.3	139096	C	A	Exon5	Non-CDS	1			NM_001058.2	1635
Tachykinin Receptor 1	TACR1	AE106s6	6	317	TGCAAGTCC [T/C] AGTGTGAGG	86	149	AC007400.3	139193	C	T	Exon5	Non-CDS	1			NM_001058.2	1538
Tachykinin Receptor 1	TACR1	AE106s7	6	611	GTCCAGGGA [C/T] GAGGGTGTG	87	150	AC007400.3	139387	C	T	Exon5	Silent	1	TCG	TCA	NM_001058.2	1344
C1 Esterase Inhibitor	C1NH	AE105s1	3	319	AAAGGACA [G/A] AGGGAAT	88	151	X54486.1	5755	G	A	Intron4	Non-CDS	0				
C1 Esterase Inhibitor	C1NH	AE105s2	6	156	ACTGTTAAG [G/A] TGCATCTCT	89	152	X54486.1	15193	A	G	Intron6	Non-CDS	0				
C1 Esterase Inhibitor	C1NH	AE105s3	5	366	CGACCAG [C/T] CAGGATATG	90	153	X54486.1	15401	C	T	Exon7	Silent	0	AGC	AGT	NM_000062.1	1278
C1 Esterase Inhibitor	C1NH	AE105s4	7	586	TGCTATTCG [T/C] TGAACCCAT	91	154	X54486.1	3493	T	C	Exon3	Missense	0	GTT	GCT	NM_000062.1	227
C1 Esterase Inhibitor	C1NH	AE105s5	7	897	CCTTCTCAG [C/G] AATGAAGAA	92	155	X54486.1	3802	C	G	Exon3	Missense	0	GCA	GGA	NM_000062.1	536
C1 Esterase Inhibitor	C1NH	AE105s6	6	276	TTCCTCTTC [A/G] TGCTCTGGG	93	156	X54486.1	18012	G	A	Exon8	Missense	0	GTG	ATG	NM_000062.1	1496
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s1	1	153	GGGCTTTTT [C/T] GCACTCATC	94	157	AF277050.1	4773	A	G	Exon4	Missense	0	AAA	GAA	NM_002257.1	592
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s2	1	299	CCCCATCCC [C/T] GCCTTGGGC	95	158	AF277050.1	4627	G	A	Intron3	Non-CDS	0				
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s3	2	605	TTGCCCACC [G/C] AGGAACCCG	96	159	AF277050.1	4532	G	C	Exon3	Missense	0	GAG	CAG	NM_002257.1	469
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s4	2	717	GGACTCCTG [C/T] GTCCAAGGG	97	160	AF277050.1	4644	C	T	Intron3	Non-CDS	0				
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s5	4	632	GGCATGAGA [C/T] TGACACAGC	98	161	AF277050.1	5693	A	G	3' Flank	Non-CDS	0				
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s6	4	697	TGGAAAGAT [G/A] GGTGATGGC	99	162	AF277050.1	5628	T	C	3' Flank	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s6	1	67	TGTCATCAA [T/C] GGGGTCAT	579	611	U48231.1	1599	C	T	Exon3	Silent	0	AAC	AAT	NM_000710.1	348
Bradykinin Receptor B1	BDKRB1	AE103s7	1	181	CGGCGGAG [G/A] CAGGCCCGG	580	612	U48231.1	1713	G	A	Exon3	Silent	0	AGG	AGA	NM_000710.1	462
Bradykinin Receptor B1	BDKRB1	AE103s8	1	296	GCCTGCATC [C/G] TGCTCCTC	581	613	U48231.1	1828	C	G	Exon3	Missense	0	CTG	GTG	NM_000710.1	577
Bradykinin Receptor B1	BDKRB1	AE103s9	2	136	ACGCGGGA [G/A] GAGGTCAGA	582	614	U48231.1	1956	G	A	Exon3	Silent	0	GAG	GAA	NM_000710.1	705
Bradykinin Receptor B2	BDKRB2	AE104s18	7	202	TGGAGAATG [C/A] GTGTATTT	583	615	AL355102.2	68174	G	T	Intron1 c	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s19	7	339	TGTCTGTT [C/T] GTGAGGACT	584	616	AL355102.2	68037	G	A	Exon2	Missense	1	CGT	TGT	NM_000623.1	40
Bradykinin Receptor B2	BDKRB2	AE104s20	2	271	CCTTCCTTC [C/A] GAAGAGAAC	585	617	AL355102.2	101076	A	C	5'Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s21	3	408	AAACACCCG [C/T] ACCCAGGAA	586	618	AL355102.2	100859	A	G	5'Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s22	3	463	GTACGTGGC [G/A] TACAAAGAA	587	619	AL355102.2	100804	T	C	5'Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s23	3	886	ATGACATCA [T/C] TACCCAGCC	588	620	AL355102.2	100381	G	A	5'Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s24	4	918	CATCATCGA [T/C] GTAATCACA	589	621	AL355102.2	63922	A	G	Exon3	Silent	1	GAT	GAC	NM_000623.1	933
Bradykinin Receptor B2	BDKRB2	AE104s25	4	1046	GCCAGAAAG [G/A] GGGCTGCAG	590	622	AL355102.2	63794	C	T	Exon3	Missense	1	GGG	GAG	NM_000623.1	1061
Bradykinin Receptor B2	BDKRB2	AE104s26	4	1543	CAGGAGAAC [T/C] GCCATCCAG	591	623	AL355102.2	63297	A	G	Exon3	Non-CDS	1			NM_000623.1	1558

Table IV (2 of 2)

GENE_DESCRIPTION	HGNC_ID	SNP_ID	CONTIG_NUM	CONTIG_POS	FLANK_SEQ [REF / ALT]	FLANK_SEQ REF (SEQ ID NO:)	FLANK_SEQ ALT (SEQ ID NO:)	REF_SEQ_ID	REF_SEQ_POS	REF_NT	ALT_NT	EXON	MUTATION_TYPE	REVCOMP	REF_CODON	ALT_CODON	CDNA_SEQ_ID	CDNA_SEQ_POS
Bradykinin Receptor B2	BDKRB2	AE104s27	4	1826	AAGTGGGAA [C/T] GACTGGGCA	592	624	AL355102.2	62978	G	A	Exon3	Non-CDS	1			NM_000623.1	1877
Bradykinin Receptor B2	BDKRB2	AE104s28	4	2102	TGAGGCATC [A/T] TTACGCAGA	593	625	AL355102.2	62738	T	A	Exon3	Non-CDS	1			NM_000623.1	2117
Bradykinin Receptor B2	BDKRB2	AE104s29	4	2239	AGGTGCTCA [T/C] TGGCTCCCT	594	626	AL355102.2	62601	A	G	Exon3	Non-CDS	1			NM_000623.1	2254
Angiotensin Converting Enzyme 2	ACE2	AE109s1	7	55	TGAAAGAA [C/A] CACATGGCC	595	627	AC003669.1	68127	C	A	Intron14	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s2	10	37	ATCATAGAT [A/G] TAAATATAT	596	628	AC003669.1	89795	C	T	Intron12	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s3	10	290	AGTTGACAA [C/G] TTTCACACC	597	629	AC003669.1	89542	C	G	Intron13	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s4	11	282	ATTAGTAGC [C/T] TACCTGGT	598	630	AC003669.1	90164	C	T	Intron3	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s5	11	440	GAATGCTAA [T/C] ATAAAGATA	599	631	AC003669.1	90322	T	C	Intron2	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s6	15	109	AGAATAATG [C/T] TTGGCACAC	600	632	AC003669.1	84113	C	T	Intron16	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s7	15	241	ATCAGACAC [A/G] TTTTTAGGT	601	633	AC003669.1	84245	A	G	Exon16	Silent	1	AAT	AAC	AF241254.1	2173
Protease Inhibitor 4	PI4	AE110s1	2	447	GCCTGCAGA [T/G] GTCCTGTAC	602	634	L26101.1	6653	T	G	Intron1	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s2	2	528	CAAAGACTT [C/T] TATGTTGAT	603	635	L26101.1	6734	C	T	Exon2	Silent	0	TTC	TTT	NM_006215.1	699
Protease Inhibitor 4	PI4	AE110s3	3	168	GAGTTAGA [A/G] CATTAG	604	636	L26101.1	7821	T	C	Intron2	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s4	3	269	CCCACAAAC [T/A] GCTTCGG	605	637	L26101.1	7720	T	A	Intron2	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s5	4	563	CTTGAGCTC [A/G] CTGACCAAATC	606	638	L26101.1	3797	T	C	Exon1	Silent	0	AGT	AGC	NM_006215.1	597
Protease Inhibitor 4	PI4	AE110s6	4	1628	GAGGATGGC [T/A] ATCCTCAGA	607	639	L26101.1	2732	A	T	5'Flank	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s7	4	1685	TCCACAAC [A/C] TCTGTGGAG	608	640	L26101.1	2695	T	G	5'Flank	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s8	4	1818	CCAAAGTTG [T/C] GGGGATAG	609	641	L26101.1	2544	A	G	5'Flank	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s9	4	2020	TGTTTGTTT [G/C] GTTGTTTGT	610	642	L26101.1	2340	C	G	5'Flank	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s24	6	383	GAGCCGGGT[A/G]AGGTCTGGT	858	884	AL023653.1	69644	C	T	Intron11	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s25	13	83	GCTAGGGGC[T/C]TCGGACCTT	859	885	AL023653.1	70696	G	A	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s26	13	161	AACAGGATG[T/C]CCCAACAGG	860	886	AL023653.1	70620	G	A	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s27	18	112	TCCAGGAAC[T/C]GAGTGCCAA	861	887	AL023653.1	65621	C	T	Intron7	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s28	21	261	CATGGTCCC[A/G]GAGAGCCC	862	888	AL023653.1	84097	G	A	Exon21	Non-CDS	0			U90724.1	2689
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s29	21	293	CCTGTTGGG[C/T]ATAGCCA	863	889	AL023653.1	84129	C	T	Exon21	Non-CDS	0			U90724.1	2601
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s30	22	144	CCCTCCAGC[A/G]GGAATCTCG	864	890	AL023653.1	61848	T	C	Exon6	Silent	0	CCT	CCC	U90724.1	711
Bradykinin Receptor B1	BDKRB1	AE103s10	7	786	ACAAGGTGC[A/G]GGGCCGGA	865	891	U48231.1	1979	G	A	Exon3	Missense	0	CGG	CAG	NM_000710.1	728
Bradykinin Receptor B1	BDKRB1	AE103s11	7	1292	GTGGGCCCT[G/A]TAATACAC	866	892	U48231.1	2504	A	G	Exon3	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s12	7	1808	CTCAAGGGC[T/G]CAAGTGATC	867	893	U48231.1	3026	T	G	Exon3	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s13	7	1946	ACAAGTATC[A/G]GGTAATGGC	868	894	U48231.1	3163	G	A	Exon3	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s14	7	1964	CCTCTCTTA[T/C]TACACTTCC	869	895	U48231.1	3181	T	C	Exon3	Non-CDS	0				
Bradykinin Receptor B2	BDKRB2	AE104s30	2	108	GTTGTGAGG[G/A]TTAAAGGCA	870	896	AL355102.2	62804	C	T	Exon3	Non-CDS	1			NM_000623.1	2051
Bradykinin Receptor B2	BDKRB2	AE104s31	3	93	GGCACGGAG[T/G]CCTCACGAA	871	897	AL355102.2	68030	T	G	Exon3	Missense	1	GAC	GCC	NM_000623.1	47
Bradykinin Receptor B2	BDKRB2	AE104s32	3	402	AACTGACCT[G/A]AGTACAGTG	872	898	AL355102.2	68339	G	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s33	3	404	CTGACCTGA[G/A]TACAGTGAA	873	899	AL355102.2	68341	G	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s34	6	348	TCTGCTCCA[T/C]GGAGCTATT	874	900	AL355102.2	62672	C	T	Exon3	Non-CDS	1			NM_000623.1	2183
Bradykinin Receptor B2	BDKRB2	AE104s35	6	364	ATTTCTAGA[C/A]CTCAGTGTC	875	901	AL355102.2	62658	C	A	Exon3	Non-CDS	1			NM_000623.1	2157
Bradykinin Receptor B2	BDKRB2	AE104s36	6	619	GACCGTCTC[G/A]TCGAACAGC	876	902	AL355102.2	62943	G	A	Exon3	Non-CDS	1			NM_000623.1	1912
Protease Inhibitor 4	PI4	AE110s10	2	397	GAACGTT[G/C]GTGGCT	877	903	L26101.1	9169	C	G	Exon4	Silent	0	ACC	ACG	NM_006215.1	1143
Protease Inhibitor 4	PI4	AE110s11	4	304	CACGC[A/G]TGTTTGC	878	904	L26101.1	3612	C	T	Exon1	Missense	0	CGC	TGC	NM_006215.1	412
Protease Inhibitor 4	PI4	AE110s12	4	1392	GGTACCC[G/A]TTTCATAA	879	905	L26101.1	2524	C	T	5' Flank	Non-CDS	0				
Tachykinin Receptor 1	TACR1	AE105s8	2	92	ATGTAGAT[A/G]GTCTTGTGG	880	906	AC007400.3	141073	G	A	Intron4	Non-CDS	1				
Tachykinin Receptor 1	TACR1	AE105s9	3	405	CCAGA[T/G]GCAGCTAG	881	907	AC007400.3	143395	C	A	Intron3	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s8	12	359	CTTGTGA[C/A]ACAGCT	882	908	AC003669.1	69476	G	T	Intron13	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s9	20	123	AAGTACA[T/C]GAAGAATT	883	909	AC003669.1	85668	C	T	Intron6	Non-CDS	1				

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GENE_DESCRIPTION	HGNC_ID	SNP_ID	CONTIG_NUM	CONTIG_POS	REFSEQ_FLANK_ORIENT	REFSEQ_FLANK	REFSEQ_FLANK REF (SEQ ID NO:)	REFSEQ ALT (SEQ ID NO:)	REF_SEQ_ID	REF_SEQ_POS	REF_NT	ALT_NT	EXON	MUTATION_TYPE	REVCOMP	REF_CODON	ALT_CODON	CDNA_SEQ_ID	CDNA_SEQ_POS
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s1	1	127	0	GATGTCAGCCTGCTGTCTCC[C/G]GAGCATGTGAGTGCCCCTCA	163	226	AL023653.1	82896	C	G	Exon20	Silent	0	CCC	CCG	U90724.1	2085
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s2	4	535	N/A	GTCTCCTTTGCAGAACAGTC[C/T]AGTGTTACACTGAGTCCAGT	164	227	AL023653.1	60150	C	T	Intron3	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s3	5	224	N/A	CCAGATTTCCCCTCACCACC[T/C]TCCCCCAAGGGGGCACCCAA	165	228	AL023653.1	74483	T	C	Intron15	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s4	5	392	1	GGCCACTGACAAGGCCTCAG[C/T]CCAAGCTGAGCCTCATCCTA	166	229	AL023653.1	74651	C	T	Intron15	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s5	6	432	1	AGAAAGGGTTGGAGTGAGGG[T/C]TGGGGCCCGAGTCTCTTTTT	167	230	AL023653.1	54549	T	C	Intron1	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s6	7	258	1	AGCACTCCCCAGGCCACCCC[C/T]CTTTTATTATACCCTCTATG	168	231	AL023653.1	75521	C	T	Intron7	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s7	10	461	N/A	TTTGTTTGAGGAAAGGGTTT[C/T]GCTGCTTTTTAAGAGGATGC	169	232	AL023653.1	65566	C	T	Intron7	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s8	13	273	1	CCTGCCAGTCCTCTGAAAAC[A/G]CCCCTGTGCCATGGAGACCT	170	233	AL023653.1	68288	A	G	Intron10	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s9	13	324	1	TAGAGAGCATTGCCACGAAA[T/C]GGTGGCAAATCTCACGTCTG	171	234	AL023653.1	68236	T	C	Intron10	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s10	14	856	0	TTGCAAACCTTAGCATGCAC[C/G]TGAGTCACCTGGGATGCTTG	172	235	AL023653.1	63068	C	G	Intron7	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s11	15	187	N/A	GAAGCCCAGGCCCCAGAGGT[C/T]CTCCCACCAAGGCCTCCCAC	173	236	AL023653.1	71620	C	T	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s12	15	194	0	AGGCCCCAGAGGTCCTCCCA[C/T]CAAGGCCTCCCACGTGACCC	174	237	AL023653.1	71627	C	T	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s13	15	218	0	GGCCTCCCACGTGACCCAGT[G/A]CAGGGTTAGGCTGCCCTTCT	175	238	AL023653.1	71651	G	A	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s14	8	221	N/A	GGAAAGGCCTGAAGGAAGAG[G/C]CCGGGGAAAGAGCCCTCCCT	176	239	AL023653.1	54358	G	C	Exon1	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s15	8	243	1	ACCCTCTGTCTGCTCGAGCC[C/T]AGGAAAGGCCTGAAGGAAGA	177	240	AL023653.1	54334	C	T	Exon1	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s16	14	139	1	CTTGCCTCAGGCAGATCAGC[A/G]TTAAATATTCCTTGTCAATT	178	241	AL023653.1	66924	A	G	Intron8	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s17	22	809	1	ACTGATACCATGTTTATGTC[T/G]TCCTTTCTAGGGCCAGTGGG	179	242	AL023653.1	77205	T	G	Intron17	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s18	22	964	1	AAATAAATAATAAAAGCCAG[A/C]GCCAATCTGGTGTGTGCCAG	180	243	AL023653.1	77052	A	C	Intron17	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s19	26	195	1	CTCCTCTGGCTCCTCCTCCC[G/A]TCCTCCATATCACCTCTTCC	181	244	AL023653.1	75689	G	A	Intron15	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s20	27	306	0	ACCTCTTGGCAGCTTGGCTT[A/G]GAGAGGCTGTCACCCCTTCT	182	245	AL023653.1	83469	A	G	Intron20	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s21	27	695	N/A	CCTATGGAGAAGGTCCCAGG[C/A]CCCAGGAACACAGGGCTTCT	183	246	AL023653.1	83858	C	A	Exon21	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s22	28	710	0	CCGGGGTTGTATACCACACC[C/G]TGGGCCCCTAATCCCAGGCC	184	247	AL023653.1	83926	C	G	Exon21	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s23	28	1369	0	CAGATGAGCCAGCATTCCAG[C/T]TCTTTCACCCTTCAGCAACA	185	248	AL023653.1	84585	C	T	Exon21	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s1	6	307	0	AATTTATGTCTTTGTGGGCC[G/A]GCTCTTCAGGACCAAGGTCT	186	249	U48231.1	2207	G	A	Exon2	Missense	0	CGG	CAG	NM_000710.1	956
Bradykinin Receptor B1	BDKRB1	AE103s2	4	273	1	CTGCTGCACAGAGTGCTGCC[G/A]ACATTTATCATCTCCATCTG	187	250	U48231.1	1360	G	A	Exon2	Silent	0	CCG	CCA	NM_000710.1	129
Bradykinin Receptor B1	BDKRB1	AE103s3	7	958	1	AGAAGCTTGGCTTTCTTATC[A/G]ATTCTTTGTGACATAATAAA	188	251	U48231.1	2355	A	G	Exon3	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s4	1	196	1	TGTTGTTGTTGAGACAGGGT[C/T]TCAGTCCGTCGGCCCAGACT	189	252	U48231.1	230	C	T	Exon1	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s5	7	240	1	ATAGTGCTAGGATTATAGGC[G/A]TGGCCACTGCGCCTGGCCCC	190	253	U48231.1	3072	G	A	Exon3	Non-CDS	0				
Bradykinin Receptor B2	BDKRB2	AE104s1	10	86	N/A	CAAATCTGCAGGGCTCCCCC[C/G]ACCGCGCCCAGGTGGGCCCC	191	254	AL355102.2	98426	C	G	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s2	10	87	0	AAATCTGCAGGGCTCCCCCC[A/G]CCGCGCCCAGGTGGGCCCCT	192	255	AL355102.2	98427	A	G	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s3	10	462	0	AAGGGCTGGCTGAGGTCATG[T/A]TCCCCCTCTGAGACTCAGTT	193	256	AL355102.2	98802	T	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s4	10	542	0	CAGGGAGAGCTGGGATGAGG[C/T]CTGGGGTGCTGCCTGTGGGG	194	257	AL355102.2	98882	C	T	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s5	10	557	0	TGAGGCCTGGGGTGCTGCCT[G/A]TGGGGACAGCACGCATGCTT	195	258	AL355102.2	98897	G	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s6	10	717	N/A	TGCTGCCAGGGCCCGAAGAC[G/A]CAGCACAGTTTTTTCTCCAG	196	259	AL355102.2	99056	G	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s7	7	408	1	GCCCTGGAGGGAGCAGGGGG[G/C]TTGTGGGACACAGACTTGGA	197	260	AL355102.2	66369	G	C	Intron2	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s8	5	275	1	GGGAACTGAGGCAGGGACAG[A/G]TGGTTGTGCAATAGTTATTG	198	261	AL355102.2	62653	A	G	Exon3	Non-CDS	1			NM_000623.1	2002
Bradykinin Receptor B2	BDKRB2	AE104s9	5	390	1	TCCCAGTTACGTCTGCGTAA[T/A]GATGCCTCACATGTACGTAG	199	262	AL355102.2	62738	T	A	Exon3	Non-CDS	1			NM_000623.1	2117
Bradykinin Receptor B2	BDKRB2	AE104s10	5	527	1	TGACAGGTGGAAGGGAGCCA[A/G]TGAGCACCTACTGTGTGCCA	200	263	AL355102.2	62601	A	G	Exon3	Non-CDS	1			NM_000623.1	2254
Bradykinin Receptor B2	BDKRB2	AE104s11	6	579	0	ATAACAGCTCATTGAGTCTT[T/G]CACAGGACAGATGTTCTTTA	201	264	AL355102.2	61132	T	G	Exon3	Non-CDS	1			NM_000623.1	3604
Bradykinin Receptor B2	BDKRB2	AE104s12	6	585	0	GCTCATTGAGTCTTTCACAG[G/T]ACAGATGTTCTTTATCAGGG	202	265	AL355102.2	61138	G	T	Exon3	Non-CDS	1			NM_000623.1	3598
Bradykinin Receptor B2	BDKRB2	AE104s13	6	727	N/A	AAGAGAGTCTCAGACCATCA[C/T]GTGCTCTGGTGCTGAATGAC	203	266	AL355102.2	61280	C	T	Exon3	Non-CDS	1			NM_000623.1	3456
Bradykinin Receptor B2	BDKRB2	AE104s14	8	482	N/A	GCCGATGGTGAACACCATTG[C/T]CATTCCTTTTCACACTCTTC	204	267	AL355102.2	62290	C	T	Exon3	Non-CDS	1			NM_000623.1	2565
Bradykinin Receptor B2	BDKRB2	AE104s16	9	1010	1	TATGGAGACAGACTAGGCAA[G/A]TTTTGTTTAATAAATGAGTG	205	268	AL355102.2	60403	G	A	3' Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s17	9	1072	1	TGAGCGATGAGCCCCAGGTT[C/T]CTGGCATGGATGGATGGATG	206	269	AL355102.2	60341	C	T	3' Flank	Non-CDS	1				
Tachykinin Receptor 1	TACR1	AE106s1	1	614	1	GCGAAGACAGCGGCGATGGG[A/G]AAGAAGTTGTGGAACTTGCA	207	270	AC007681.3	103685	A	G	Exon1	Silent	1	TTT	TTC	NM_001058.2	543
Tachykinin Receptor 1	TACR1	AE106s2	2	789	N/A	AGCAGGAGAGCCAGGACCCA[G/T]ATGACACAGATGACCACTTT	208	271	AC007681.3	25759	G	T	Exon2	Silent	1	ATC	ATA	NM_001058.2	672
Tachykinin Receptor 1	TACR1	AE106s3	4	676	0	GGGTGGGTTAGTTCTGCCTG[T/G]CCCCTGCTCACCTTGCGCTT	209	272	AC007400.3	143458	T	G	Intron3	Non-CDS	1				
Tachykinin Receptor 1	TACR1	AE106s4	6	152	0	CAGAATGGAATGAATGGGCT[T/C]TGGGAAAAGCTGGTCCGAC	210	273	AC007400.3	139028	T	C	Exon5	Non-CDS	1				
Tachykinin Receptor 1	TACR1	AE106s5	6	220	0	CAGTGATTTGGTTTGAGTCA[C/A]ACAGCATGAGGGTGGCAAAG	211	274	AC007400.3	139096	C	A	Exon5	Non-CDS	1			NM_001058.2	1635
Tachykinin Receptor 1	TACR1	AE106s6	6	317	N/A	CTGACCCTTTTTGCAAGTCC[C/T]AGTGTGAGGGTGTTTCTGAT	212	275	AC007400.3	139193	C	T	Exon5	Non-CDS	1			NM_001058.2	1538
Tachykinin Receptor 1	TACR1	AE106s7	6	511	0	TTGGAGGTCAGGTCCAGGGA[C/T]GAGGGTGTGGCCTTGGGGCC	213	276	AC007400.3	139387	C	T	Exon5	Silent	1	TCG	TCA	NM_001058.2	1344
C1 Esterase Inhibitor	C1NH	AE105s1	3	319	0	CGCTGGGGAAAGAAAGGACA[G/A]AGGGAATGTTGGAGCTACAG	214	277	X54486.1	5755	G	A	Intron4	Non-CDS	0				
C1 Esterase Inhibitor	C1NH	AE105s2	5	158	0	GCGGTAGGAAGACTGTTAAG[A/G]TGCATCTCTTATTTTCTAGG	215	278	X54486.1	15193	A	G	Intron6	Non-CDS	0				
C1 Esterase Inhibitor	C1NH	AE105s3	5	366	0	CGCATCAAAGTGACGACCAG[C/T]CAGGATATGCTCTCAATCAT	216	279	X54486.1	15401	C	T	Exon7	Silent	0	AGC	AGT	NM_000062.1	1278
C1 Esterase Inhibitor	C1NH	AE105s4	7	598	0	TATCTCCAAGATGCTATTCG[T/C]TGAACCCATCCTGGAGGTTT	217	280	X54486.1	3493	T	C	Exon3	Missense	0	GTT	GCT	NM_000062.1	227
C1 Esterase Inhibitor	C1NH	AE105s5	7	897	0	GCTCTACCACGCCTTCTCAG[C/G]AATGAAGAAGGTGGAGACCA	218	281	X54486.1	3802	C	G	Exon3	Missense	0	GCA	GGA	NM_000062.1	536
C1 Esterase Inhibitor	C1NH	AE105s6	8	278	N/A	TGCAGCAGCCCTTCCTCTTC[G/A]TGCTCTGGGACCAGCAGCAC	219	282	X54486.1	18012	G	A	Exon8	Missense	0	GTG	ATG	NM_000062.1	1498
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s1	1	153	1	TCCTGCCTAATGATGAGTGC[A/G]AAAAAGCCCACGTCCAGAAG	220	283	AF277050.1	4773	A	G	Exon4	Missense	0	AAA	GAA	NM_002257.1	592
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s2	1	299	1	CAGACTGTGTAGCCCAAGGC[G/A]GGGATGGGGACTCCTGCGTC	221	284	AF277050.1	4627	G	A	Intron3	Non-CDS	0				
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s3	2	605	0	AGGTCGTGGAGTTGCCCACC[G/C]AGGAACCCGAAGTGGGGAGC	222	285	AF277050.1	4532	G	C	Exon3	Missense	0	GAG	CAG	NM_002257.1	469
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s4	2	717	0	GGCGGGGATGGGGACTCCTG[C/T]GTCCAAGGGAGAAAGGGCCA	223	286	AF277050.1	4644	C	T	Intron3	Non-CDS	0				
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s5	4	632	1	GGGCCACCCCAGCTGTGTCA[A/G]TTCTCATGCCTGGAAGTCTGA	224	287	AF277050.1	5693	A	G	3' Flank	Non-CDS	0				
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s6	4	697	1	TGTCACGTTCTGCCATCACC[T/C]ATCTTTCCAGATGTGGTGCA	225	288	AF277050.1	5628	T	C	3' Flank	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s6	1	67	N/A	CTCCTCTGCCGTGTCATCAA[C/T]GGGGTCATCAAGGCCAATTT	643	675	U48231.1	1599	C	T	Exon3	Silent	0	AAC	AAT	NM_000710.1	348
Bradykinin Receptor B1	BDKRB1	AE103s7	1	181	0	GGAAGGCAGCAGCGGCGGAG[G/A]CAGGCCCGGGTCACCTGCGT	644	676	U48231.1	1713	G	A	Exon3	Silent	0	AGG	AGA	NM_000710.1	462
Bradykinin Receptor B1	BDKRB1	AE103s8	1	296	0	TGAACATCACCGCCTGCATC[C/G]TGCTCCTCCCCCATGAGGCC	645	677	U48231.1	1828	C	G	Exon3	Missense	0	CTG	GTG	NM_000710.1	577

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Bradykinin Receptor B1	BDKRB1	AE103s9	2	136	0	GCCTCCCTGCGAACGCGGGA[G/A]GAGGTCAGCAGGACAAGAGT	646	678	U48231.1	1956	G	A	Exon3	Silent	0	GAG	GAA	NM_000710.1	705
GENE_DESCRIPTION	HGNC_ID	SNP_ID	CONTIG_NUM	CONTIG_POS	REFSEQ_FLANK_ORIENT	REFSEQ_FLANK	REFSEQ_FLANK REF (SEQ ID NO:)	REFSEQ ALT (SEQ ID NO:)	REF_SEQ_ID	REF_SEQ_POS	REF_NT	ALT_NT	EXON	MUTATION_TYPE	REVCOMP	REF_CODON	ALT_CODON	CDNA_SEQ_ID	CDNA_SEQ_POS
Bradykinin Receptor B2	BDKRB2	AE104s18	7	202	1	CTGGGGATTGCAAAATACAC[G/T]CATTCTCCAGCAGGGAGGAG	647	679	AL355102.2	68174	G	T	Intron1 o	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s19	7	339	1	GGTGGGCACGGAGTCCTCAC[G/A]AACAGACAGAAACATTGATA	648	680	AL355102.2	68037	G	A	Exon2	Missense	1	CGT	TGT	NM_000623.1	40
Bradykinin Receptor B2	BDKRB2	AE104s20	2	271	N/A	AGCCTTAAAACCCTTCCTTC[A/C]GAAGAGAACAGATAAGAGTG	649	681	AL355102.2	101076	A	C	5'Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s21	3	408	1	AGCTGTCCTGTTTCCTGGGT[A/G]CGGGTGTTTGCGCTCCCCTG	650	682	AL355102.2	100850	A	G	5'Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s22	3	463	1	AGTCCTGGGATTTCTTTGTA[T/C]GCCACGTACGGCTCCCAAGG	651	683	AL355102.2	100804	T	C	5 Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s23	3	886	1	CATCTTTCAAGGGATGGGTA[G/A]TGATGTCATCAGCCTCCTGG	652	684	AL355102.2	100381	G	A	5'Flank	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s24	4	916	1	GAGGCGATCTGTGTGATTAC[A/G]TCGATGATGCGCTCGTCCTG	653	685	AL355102.2	63922	A	G	Exon3	Silent	1	GAT	GAC	NM_000623.1	933
Bradykinin Receptor B2	BDKRB2	AE104s25	4	1046	1	TGGGTTCTGACCTGCAGCCC[C/T]CTTTCTGGCACACTCCCTGG	654	686	AL355102.2	63794	C	T	Exon3	Missense	1	GGG	GAG	NM_000623.1	1061
Bradykinin Receptor B2	BDKRB2	AE104s26	4	1543	1	TTGCACCAAAGCTGGATGGC[A/G]GTTCTCCTGGAGATCTAAGT	655	687	AL355102.2	63297	A	G	Exon3	Non-CDS	1			NM_000623.1	1558
Bradykinin Receptor B2	BDKRB2	AE104s27	4	1826	1	GGTGGTGGCAGTGCCCAGTC[G/A]TTCCCACTTGAGTCTTTGAG	656	688	AL355102.2	62978	G	A	Exon3	Non-CDS	1			NM_000623.1	1677
Bradykinin Receptor B2	BDKRB2	AE104s28	4	2102	1	TCCCAGTTACGTCTGCGTAA[T/A]GATGCCTCACATGTACGTAG	657	689	AL355102.2	62738	T	A	Exon3	Non-CDS	1			NM_000623.1	2117
Bradykinin Receptor B2	BDKRB2	AE104s29	4	2239	1	TGACAGGTGGAAGGGAGCCA[A/G]TGAGCACCTACTGTGTGCCA	658	690	AL355102.2	62601	A	G	Exon3	Non-CDS	1			NM_000623.1	2254
Angiotensin Converting Enzyme 2	ACE2	AE109s1	7	55	0	ACTTATAGTTTTGAAAAGAA[C/A]CACATGGCCTCTCTTCTTTC	659	691	AC003689.1	68127	C	A	Intron14	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s2	10	37	1	TCCAGATGTACATATATTTA[C/T]ATCTATGATCTATGGTTTCT	660	692	AC003689.1	69795	C	T	Intron12	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s3	10	290	1	GACAAGGAATGGGTGTGAAA[C/G]TTGTCAACTGGGTGTACTCA	661	693	AC003689.1	69542	C	G	Intron13	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s4	11	282	0	CACTACTAAAAATTAGTAGC[C/T]TACCTGGTTCAAGTAATAAG	662	694	AC003689.1	90184	C	T	Intron3	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s5	11	440	0	TTTGCTGAAGAGAATGCTAA[T/C]ATAAAGATATCCTTTTGACC	663	695	AC003689.1	90322	T	C	Intron2	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s6	15	109	0	GTAAATGACTCAGAATAATG[C/T]TTGGCACACAGGAAGAACAC	664	696	AC003689.1	64113	C	T	Intron16	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s7	15	241	0	CTAGGAATGATATCAGACAC[A/G]TTTTTAGGTGCAGTGACAAA	665	697	AC003689.1	64245	A	G	Exon16	Silent	1	AAT	AAC	AF241254.1	2173
Protease Inhibitor 4	PI4	AE110s1	2	447	0	CTAGCTCTGTGGCCTGCAGA[T/G]GTCCTGTACCTTCTTTTCAT	666	698	L28101.1	6653	T	G	Intron1	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s2	2	528	0	AGGACCACTCCCAAAGACTT[C/T]TATGTTGATGAGAACACAAC	667	699	L28101.1	6734	C	T	Exon2	Silent	0	TTC	TTT	NM_006215.1	699
Protease Inhibitor 4	PI4	AE110s3	3	168	1	GCTTGTTCATTAATCTAATG[T/C]TCTAACTCAATGCCCCTTTC	668	700	L28101.1	7821	T	C	Intron2	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s4	3	269	1	GAGGTGGTCTGAGCCGAAGC[T/A]GTTTGTGGGGACAGAACTCA	669	701	L28101.1	7720	T	A	Intron2	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s5	4	563	1	AAGATTGTGGATTTGGTCAG[T/C]GAGCTCAAGAAGGACGTCTT	670	702	L28101.1	3797	T	C	Exon1	Silent	0	AGT	AGC	NM_006215.1	597
Protease Inhibitor 4	PI4	AE110s6	4	1628	1	CTAAAATAAACTCTGAGGAT[A/T]GCCATCCTCCATGCAAAATC	671	703	L28101.1	2732	A	T	5'Flank	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s7	4	1665	1	CATATAAAGCACTCCACAGA[T/G]GTTTGTGGAACAGACCCTAA	672	704	L28101.1	2695	T	G	5'Flank	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s8	4	1816	1	CGGGTACCAATTCTATCCCC[A/G]CAACTTTGGGCAGGTCACTT	673	705	L28101.1	2544	A	G	5'Flank	Non-CDS	0				
Protease Inhibitor 4	PI4	AE110s9	4	2020	1	CAAACAAACAAACAAACAAC[C/G]AAACAAACAAAAAAAACCCA	674	706	L28101.1	2340	C	G	5'Flank	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s24	6	363	1	CTGTGGCTGCAACCAGACCT[C/T]ACCCGGCTCCTCTGTTTCCC	910	936	AL023653.1	69644	C	T	Intron11	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s25	13	83	1	AGTCCACGTTGAAGGTCCGA[G/A]GCCCCTAGCCCTGTGGGGGC	911	937	AL023653.1	70698	G	A	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s26	13	161	1	TTTTCTAGGGCCCTGTTGGG[G/A]CATCCTGTTGTGTGTGTAGA	912	938	AL023653.1	70620	G	A	Intron13	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s27	18	112	0	AAGGCTGACCTTCCAGGAAC[C/T]GAGTGCCAAAGGCAAGGTCT	913	939	AL023653.1	65621	C	T	Intron7	Non-CDS	0				
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s28	21	261	0	CCCAAGGGTGCCATGGTCCC[G/A]GGAGAGCCCAAACCTATCAC	914	940	AL023653.1	84097	G	A	Exon21	Non-CDS	0			U90724.1	2689
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s29	21	293	0	ACCTATCACCACCTGTTGGG[C/T]ATAGCCAGAGCTGTTCCCAC	915	941	AL023653.1	84129	C	T	Exon21	Non-CDS	0			U90724.1	2801
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s30	22	144	1	TGGCTCCTCACCGAGATTCC[T/C]GCTGGAGGGCGTGTGGGTTT	916	942	AL023653.1	61848	T	C	Exon6	Silent	0	CCT	CCC	U90724.1	711
Bradykinin Receptor B1	BDKRB1	AE103s10	7	766	0	GGTCAGCAGGACAAGAGTGC[G/A]GGGGCCGAAGGATAGCAAGA	917	943	U48231.1	1079	G	A	Exon3	Missense	0	CGG	CAG	NM_000710.1	728
Bradykinin Receptor B1	BDKRB1	AE103s11	7	1292	0	GAATTATCCAAGTGGGCCCT[A/G]TATAATCACAAGGGTCCTTA	918	944	U48231.1	2504	A	G	Exon3	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s12	7	1808	0	CTGGTCTCAAACTCAAGGGC[T/G]CAAGTGATCCTCCACTTTGG	919	945	U48231.1	3026	T	G	Exon3	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s13	7	1946	0	GGAAACAAATAACAAGTATC[G/A]GGTAATGGCCTCTCTTATTA	920	946	U48231.1	3163	G	A	Exon3	Non-CDS	0				
Bradykinin Receptor B1	BDKRB1	AE103s14	7	1964	0	TCGGGTAATGGCCTCTCTTA[T/C]TACACTTCCATTTGTCTATT	921	947	U48231.1	3181	T	C	Exon3	Non-CDS	0				
Bradykinin Receptor B2	BDKRB2	AE104s30	2	106	1	ATACCTGTTACTGCCTTTAA[C/T]CCTCACAACGACTTCATGTT	922	948	AL355102.2	62804	C	T	Exon3	Non-CDS	1			NM_000623.1	2051
Bradykinin Receptor B2	BDKRB2	AE104s31	3	93	0	AGGCCGTGGTGGGCACGGAG[T/G]CCTCACGAACAGACAGAAAC	923	949	AL355102.2	68030	T	G	Exon3	Missense	1	GAC	GCC	NM_000623.1	47
Bradykinin Receptor B2	BDKRB2	AE104s32	3	402	0	TAATAACTGCAAACTGACCT[G/A]AGTACAGTGAAAAATCAAGC	924	950	AL355102.2	68339	G	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s33	3	404	0	ATAACTGCAAACTGACCTGA[G/A]TACAGTGAAAAATCAAGCAA	925	951	AL355102.2	68341	G	A	Intron1	Non-CDS	1				
Bradykinin Receptor B2	BDKRB2	AE104s34	6	348	0	CCAATACTGATTCTGCTCCA[C/T]GGAGCTATTTCTAGACCTCA	926	952	AL355102.2	62672	C	T	Exon3	Non-CDS	1			NM_000623.1	2183
Bradykinin Receptor B2	BDKRB2	AE104s35	6	364	0	TCCACGGAGCTATTTCTAGA[C/A]CTCAGTGTCTTTTCCTTATA	927	953	AL355102.2	62688	C	A	Exon3	Non-CDS	1			NM_000623.1	2167
Bradykinin Receptor B2	BDKRB2	AE104s36	6	619	0	GCACCCTGCTCGACCGTCTC[G/A]TCGAACAGCTTTCTGGTGGT	928	954	AL355102.2	62943	G	A	Exon3	Non-CDS	1			NM_000623.1	1912
Protease Inhibitor 4	PI4	AE110s10	2	397	1	ACCGAGGCTGCAGCAGCCAC[C/G]ACGTTCGCGATCAAATTCTT	929	955	L28101.1	9169	C	G	Exon4	Silent	0	ACC	ACG	NM_006215.1	1143
Protease Inhibitor 4	PI4	AE110s11	4	304	1	CCGGCCATGGGCTGGAAACA[C/T]GCGTGGGCAGTGCTCTGTTC	930	956	L28101.1	3612	C	T	Exon1	Missense	0	CGC	TGC	NM_006215.1	412
Protease Inhibitor 4	PI4	AE110s12	4	1392	1	GACAGATGTTCATTATGAAA[C/T]GGGTACCAATTCTATCCCCA	931	957	L28101.1	2524	C	T	5' Flank	Non-CDS	0				
Tachykinin Receptor 1	TACR1	AE106s8	2	92	0	TGGCCACTGTGTATGTAGAT[G/A]GTCTTGTGGCCCCTGGAGAG	932	958	AC007400.3	141073	G	A	Intron4	Non-CDS	1				
Tachykinin Receptor 1	TACR1	AE106s9	3	406	1	GGATATTTTGTGCTAGCTGC[C/A]TCTGGGGCTCACAAGTGTGC	933	959	AC007400.3	143386	C	A	Intron3	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s8	12	359	1	AAAGAAACATTCTCAGCTGT[G/T]TCACAAGTCCTCATGAGACT	934	960	AC003689.1	69475	G	T	Intron13	Non-CDS	1				
Angiotensin Converting Enzyme 2	ACE2	AE109s9	20	123	0	ATAACAAAGAGCCAAGTACA[C/T]GAAGAATTCATGGGGCTTCT	935	961	AC003689.1	85668	C	T	Intron6	Non-CDS	1				
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s2	1	299	0	GACGCAGGAGTCCCCATCC [C/T] CGCCTTGGGCTACACAGTCTG	1574	1575	AF277050.1	4627	G	A	Intron3	Non-CDS	N/A				

Table VI

GENE_DESCRIPTION	HGNC_ID	SNP_ID	CONTIG_NUM	CONTIG_POS	REF_AA	ALT_AA	EXON	MUTATION_TYPE	REVCOMP	REF_CODON	ALT_CODON	PROTEIN_ID	PROTEIN_POS	PROTEIN (SEQ ID NO:)	FLANK_SEQ REF (SEQ ID NO:)	FLANK_SEQ ALT (SEQ ID NO:)	REFSEQ_FLANK REF (SEQ ID NO:)
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s1	1	127	P	P	Exon20	Silent	0	CCC	CCG	AAB96394.1	607	4	37	100	163
Bradykinin Receptor B1	BDKRB1	AE103s1	6	307	R	Q	Exon2	Missense	0	CGG	CAG	NP_000701.1	317	8	60	123	186
Bradykinin Receptor B1	BDKRB1	AE103s2	4	273	P	P	Exon2	Silent	0	CCG	CCA	NP_000701.1	41	10	61	124	187
Tachykinin Receptor 1	TACR1	AE106s1	1	614	F	F	Exon1	Silent	1	TTT	TTC	NP_001049.1	111	16	81	144	207
Tachykinin Receptor 1	TACR1	AE106s2	2	789	I	I	Exon2	Silent	1	ATC	ATA	NP_001049.1	154	18	82	145	208
Tachykinin Receptor 1	TACR1	AE106s7	6	511	S	S	Exon5	Silent	1	TCG	TCA	NP_001049.1	378	20	87	150	213
C1 Esterase Inhibitor	C1NH	AE105s3	5	366	S	S	Exon7	Silent	0	AGC	AGT	NP_000053.1	406	24	90	153	216
C1 Esterase Inhibitor	C1NH	AE105s4	7	588	V	A	Exon3	Missense	0	GTT	GCT	NP_000053.1	58	26	91	154	217
C1 Esterase Inhibitor	C1NH	AE105s5	7	897	A	G	Exon3	Missense	0	GCA	GGA	NP_000053.1	159	28	92	155	218
C1 Esterase Inhibitor	C1NH	AE105s6	8	276	V	M	Exon8	Missense	0	GTG	ATG	NP_000053.1	480	30	93	156	219
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s1	1	153	K	E	Exon4	Missense	0	AAA	GAA	NP_002248.1	186	34	94	157	220
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s3	2	605	E	Q	Exon3	Missense	0	GAG	CAG	NP_002248.1	145	36	96	159	222
Bradykinin Receptor B1	BDKRB1	AE103s6	1	67	N	N	Exon3	Silent	0	AAC	AAT	NP_000701.1	114	556	579	611	643
Bradykinin Receptor B1	BDKRB1	AE103s7	1	181	R	R	Exon3	Silent	0	AGG	AGA	NP_000701.1	152	558	580	612	644
Bradykinin Receptor B1	BDKRB1	AE103s8	1	296	L	V	Exon3	Missense	0	CTG	GTG	NP_000701.1	191	560	581	613	645
Bradykinin Receptor B1	BDKRB1	AE103s9	2	136	E	E	Exon3	Silent	0	GAG	GAA	NP_000701.1	233	562	582	614	646
Bradykinin Receptor B2	BDKRB2	AE104s19	7	339	R	C	Exon2	Missense	1	CGT	TGT	NP_000614.1	14	564	584	616	648
Bradykinin Receptor B2	BDKRB2	AE104s24	4	918	D	D	Exon3	Silent	1	GAT	GAC	NP_000614.1	311	566	589	621	653
Bradykinin Receptor B2	BDKRB2	AE104s25	4	1046	G	E	Exon3	Missense	1	GGG	GAG	NP_000614.1	354	568	590	622	654
Angiotensin Converting Enzyme 2	ACE2	AE109s7	15	241	N	N	Exon16	Silent	1	AAT	AAC	AAF78220.1	690	843	601	633	665
Protease Inhibitor 4	PI4	AE110s2	2	528	F	F	Exon2	Silent	0	TTC	TTT	NP_006206.1	233	574	603	635	667
Protease Inhibitor 4	PI4	AE110s5	4	563	S	S	Exon1	Silent	0	AGT	AGC	NP_006206.1	199	576	606	638	670

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Table VIIA

DNA panel	Coriell Catalog #	Sample Description	XPNPEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	PI4	ACE2
Coriell 24 panel	NA14905	African American	X	X	X	X	X			
Coriell 24 panel	NA14922	African American	X	X	X	X	X			
Coriell 24 panel	NA14923	African American	X	X	X	X	X			
Coriell 24 panel	NA14924	African American	X	X	X	X	X			
Coriell 24 panel	NA14925	African American	X	X	X	X	X			
Coriell 24 panel	NA14932	African American	X	X	X	X	X			
Coriell 24 panel	NA14933	African American	X	X	X	X	X			
Coriell 24 panel	NA14934	African American	X	X	X	X	X			
Coriell 24 panel	NA 17201	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17202	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17203	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17204	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17205	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17206	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17207	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA17208	Caucasian	X	X	X	X	X			
Coriell 24 panel	NA00576	Chinese	X	X	X	X	X			
Coriell 24 panel	NA03433	Chinese	X	X	X	X	X			
Coriell 24 panel	NA06090	Chinese	X	X	X	X	X			
Coriell 24 panel	NA07426	Chinese	X	X	X	X	X			
Coriell 24 panel	NA02345b	Japanese	X	X	X	X	X			
Coriell 24 panel	NA11589	Japanese	X	X	X	X	X			
Coriell 24 panel	NA14819	Japanese	X	X	X	X	X			
Coriell 24 panel	NA04535	Japanese	X	X	X	X	X			
Coriell 8 panel	NA14672	African American								
Coriell 8 panel	NA14682	African American								
Coriell 8 panel	NA14683	African American								
Coriell 8 panel	NA14696	African American								
Coriell 8 panel	NA14698	African American								
Coriell 8 panel	NA14700	African American								
Coriell 8 panel	NA14704	African American								
HD 50 AA panel	NA1850	African American								
HD 50 AA panel	3382	African American								
HD 50 AA panel	3725	African American								
HD 50 AA panel	6865	African American								
HD 50 AA panel	7754	African American								
HD 50 AA panel	10251	African American								
HD 50 AA panel	10378	African American								
HD 50 AA panel	12931	African American								
HD 50 AA panel	13294	African American								
HD 50 AA panel	14439	African American								
HD 50 AA panel	14441	African American								
HD 50 AA panel	14454	African American								
HD 50 AA panel	14464	African American								

Table VIIB

DNA panel	Coriell Catalog #	Sample Description	XPNPEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	PI4	ACE2
HD 50 AA panel	14537	African American	X							
HD 50 AA panel	14583	African American	X							
HD 50 AA panel	14681	African American	X							
HD 50 AA panel	14687	African American	X							
HD 50 AA panel	14697	African American	X							
HD 50 AA panel	14699	African American	X							
HD 50 AA panel	14720	African American	X							
HD 50 AA panel	14746	African American	X							
HD 50 AA panel	14754	African American	X							
HD 50 AA panel	14755	African American	X							
HD 50 AA panel	14771	African American	X							
HD 50 AA panel	14772	African American	X							
HD 50 AA panel	14783	African American	X							
HD 50 AA panel	14826	African American	X							
HD 50 AA panel	14837	African American	X							
HD 50 AA panel	14862	African American	X							
HD 50 AA panel	14863	African American	X							
HD 50 AA panel	14864	African American	X							
HD 50 AA panel	14892	African American	X							
HD 50 AA panel	14893	African American	X							
HD 50 AA panel	14894	African American	X							
HD 50 AA panel	14895	African American	X							
HD 50 AA panel	14897	African American	X							
HD 50 AA panel	14900	African American	X							
HD 50 AA panel	14901	African American	X							
HD 50 AA panel	14903	African American	X							
HD 50 AA panel	14904	African American	X							
HD 50 AA panel	14905	African American	X							
HD 50 AA panel	14922	African American	X							
HD 50 AA panel	14923	African American	X							
HD 50 AA panel	14924	African American	X							
HD 50 AA panel	14925	African American	X							
HD 50 AA panel	14932	African American	X							
HD 50 AA panel	14933	African American	X							
HD 100 CAU panel	NA 17201	Caucasian		X						
HD 100 CAU panel	17202	Caucasian		X						
HD 100 CAU panel	17203	Caucasian		X						
HD 100 CAU panel	17204	Caucasian		X						
HD 100 CAU panel	17205	Caucasian		X						
HD 100 CAU panel	17206	Caucasian		X						
HD 100 CAU panel	17207	Caucasian		X						
HD 100 CAU panel	17208	Caucasian		X						
HD 100 CAU panel	17209	Caucasian		X						
HD 100 CAU panel	17210	Caucasian		X						

Table VIIC

DNA panel	Coriell Catalog #	Sample Description	XPNPEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	PI4	ACE2
HD 100 CAU panel	17211	Caucasian		X						
HD 100 CAU panel	17212	Caucasian		X						
HD 100 CAU panel	17213	Caucasian		X						
HD 100 CAU panel	17214	Caucasian		X						
HD 100 CAU panel	17215	Caucasian		X						
HD 100 CAU panel	17216	Caucasian		X						
HD 100 CAU panel	17217	Caucasian		X						
HD 100 CAU panel	17218	Caucasian		X						
HD 100 CAU panel	17219	Caucasian		X						
HD 100 CAU panel	17220	Caucasian		X						
HD 100 CAU panel	17221	Caucasian		X						
HD 100 CAU panel	17222	Caucasian		X						
HD 100 CAU panel	17223	Caucasian		X						
HD 100 CAU panel	17224	Caucasian		X						
HD 100 CAU panel	17225	Caucasian		X						
HD 100 CAU panel	17226	Caucasian		X						
HD 100 CAU panel	17227	Caucasian		X						
HD 100 CAU panel	17228	Caucasian		X						
HD 100 CAU panel	17229	Caucasian		X						
HD 100 CAU panel	17230	Caucasian		X						
HD 100 CAU panel	17231	Caucasian		X						
HD 100 CAU panel	17232	Caucasian		X						
HD 100 CAU panel	17233	Caucasian		X						
HD 100 CAU panel	17234	Caucasian		X						
HD 100 CAU panel	17235	Caucasian		X						
HD 100 CAU panel	17236	Caucasian		X						
HD 100 CAU panel	17237	Caucasian		X						
HD 100 CAU panel	17238	Caucasian		X						
HD 100 CAU panel	17239	Caucasian		X						
HD 100 CAU panel	17240	Caucasian		X						
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HD 100 CAU panel	17242	Caucasian		X						
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HD 100 CAU panel	17245	Caucasian		X						
HD 100 CAU panel	17246	Caucasian		X						
HD 100 CAU panel	17247	Caucasian		X						
HD 100 CAU panel	17248	Caucasian		X						
HD 100 CAU panel	17249	Caucasian		X						
HD 100 CAU panel	17250	Caucasian		X						
HD 100 CAU panel	17251	Caucasian		X						
HD 100 CAU panel	17252	Caucasian		X						
HD 100 CAU panel	17253	Caucasian		X						
HD 100 CAU panel	17254	Caucasian		X						

Table VIID

DNA panel	Coriell Catalog #	Sample Description	XPNPEP2	BDKRB1	BDKRB2	TACR1	C1NH	KLK1	PI4	ACE2
HD 100 CAU panel	17255	Caucasian		X						
HD 100 CAU panel	17256	Caucasian		X						
HD 100 CAU panel	17257	Caucasian		X						
HD 100 CAU panel	17258	Caucasian		X						
HD 100 CAU panel	17259	Caucasian		X						
HD 100 CAU panel	17260	Caucasian		X						
HD 100 CAU panel	17261	Caucasian		X						
HD 100 CAU panel	17262	Caucasian		X						
HD 100 CAU panel	17263	Caucasian		X						
HD 100 CAU panel	17264	Caucasian		X						
HD 100 CAU panel	17265	Caucasian		X						
HD 100 CAU panel	17266	Caucasian		X						
HD 100 CAU panel	17267	Caucasian		X						
HD 100 CAU panel	17268	Caucasian		X						
HD 100 CAU panel	17269	Caucasian		X						
HD 100 CAU panel	17270	Caucasian		X						
HD 100 CAU panel	17271	Caucasian		X						
HD 100 CAU panel	17272	Caucasian		X						
HD 100 CAU panel	17273	Caucasian		X						
HD 100 CAU panel	17274	Caucasian		X						
HD 100 CAU panel	17275	Caucasian		X						
HD 100 CAU panel	17276	Caucasian		X						
HD 100 CAU panel	17277	Caucasian		X						
HD 100 CAU panel	17278	Caucasian		X						
HD 100 CAU panel	17279	Caucasian		X						
HD 100 CAU panel	17280	Caucasian		X						
HD 100 CAU panel	17281	Caucasian		X						
HD 100 CAU panel	17282	Caucasian		X						
HD 100 CAU panel	17283	Caucasian		X						
HD 100 CAU panel	17284	Caucasian		X						
HD 100 CAU panel	17285	Caucasian		X						
HD 100 CAU panel	17286	Caucasian		X						
HD 100 CAU panel	17287	Caucasian		X						
HD 100 CAU panel	17288	Caucasian		X						
HD 100 CAU panel	17289	Caucasian		X						
HD 100 CAU panel	17290	Caucasian		X						
HD 100 CAU panel	17291	Caucasian		X						
HD 100 CAU panel	17292	Caucasian		X						
HD 100 CAU panel	17293	Caucasian		X						
HD 100 CAU panel	17294	Caucasian		X						
HD 100 CAU panel	17295	Caucasian		X						
Omapatrilat Trial Samples	12 angioedema patients		X	X	X	X	X	X	X	X

Table VIII (1 of 2)

GENE_DESCRIPTION	HGNC_ID	SNP_ID	EXON	REVCOMP	PCR Amplicon_Name	Target_Name	PCR Left primer	PCR Left primer (SEQ ID NO:)	PCR Right primer	PCR Right primer (SEQ ID NO:)
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s1	Exon20	0	AE100p77p78	XPNPEP2_X20a	AGTGCTCCTTCCTTCCCTTC	297	TATTCACTACCTGGGGTTGGG	360
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s2	Intron3	0	AE100p9p10	XPNPEP2_X3a	CAGCCCAGGCATCTTAATCTA	298	TCTCTACTTCCCTCCCTTTGC	361
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s3	Intron15	0	AE100p57p58	XPNPEP2_X15a	TAGCTGTCTTCTTCCTTTCGC	299	ATAGGATGAGGCTCAGCTTGG	362
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s4	Intron15	0	AE100p57p58	XPNPEP2_X15a	TAGCTGTCTTCTTCCTTTCGC	300	ATAGGATGAGGCTCAGCTTGG	363
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s5	Intron1	0	AE100p1p2	XPNPEP2_X1a	TGATTGAGACCAGCTGTTGTG	301	AACAGAAAAAGAGACTCGGGC	364
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s6	Intron7	0	AE100p25p26	XPNPEP2_X7a	CCAGCGTGGGCATACATG	302	GGCCCTGAAATCTGCATTT	365
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s7	Intron7	0	AE100p25p26	XPNPEP2_X7a	CCAGCGTGGGCATACATG	303	GGCCCTGAAATCTGCATTT	366
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s8	Intron10	0	AE100p37p38	XPNPEP2_X10a	CTTCCTTTGACCTCCAGGAAC	304	CCTGTTTCCTCTTCTGGCTCT	367
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s9	Intron10	0	AE100p37p38	XPNPEP2_X10a	CTTCCTTTGACCTCCAGGAAC	305	CCTGTTTCCTCTTCTGGCTCT	368
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s10	Intron7	0	AE100p25p26	XPNPEP2_X7a	CCAGCGTGGGCATACATG	306	GGCCCTGAAATCTGCATTT	369
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s11	Intron13	0	AE100p49p50	XPNPEP2_X13a	TAAATGACAGGTCAGGGCTTG	307	CAGCTCTCAGGCCTTTTCATT	370
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s12	Intron13	0	AE100p49p50	XPNPEP2_X13a	TAAATGACAGGTCAGGGCTTG	308	CAGCTCTCAGGCCTTTTCATT	371
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s13	Intron13	0	AE100p49p50	XPNPEP2_X13a	TAAATGACAGGTCAGGGCTTG	309	CAGCTCTCAGGCCTTTTCATT	372
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s14	Exon1	0	AE100p1p2	XPNPEP2_X1a	TGATTGAGACCAGCTGTTGTG	310	AACAGAAAAAGAGACTCGGGC	373
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s15	Exon1	0	AE100p1p2	XPNPEP2_X1a	TGATTGAGACCAGCTGTTGTG	311	AACAGAAAAAGAGACTCGGGC	374
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s16	Intron8	0	AE100p29p30	XPNPEP2_X8a	GGCCCATGTCATTAATGAGTAC	312	TCAGGGCTACCTTTTGTCCTT	375
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s17	Intron17	0	AE100p65p66	XPNPEP2_X17a	CCCTCTTCTTAGGCACCACTC	313	CTGCTGGCATTCCTCACTTAC	376
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s18	Intron17	0	AE100p65p66	XPNPEP2_X17a	CCCTCTTCTTAGGCACCACTC	314	CTGCTGGCATTCCTCACTTAC	377
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s19	Intron15	0	AE100p57p58	XPNPEP2_X15a	TAGCTGTCTTCTTCCTTTCGC	315	ATAGGATGAGGCTCAGCTTGG	378
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s20	Intron21	0	AE100p81p82	XPNPEP2_X21.f1a	GGACTATGGTGACAGCTGGAG	316	CAAGAAGCCCTGTGTTCCTG	379
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s21	Exon21	0	AE100p81p82	XPNPEP2_X21.f1a	GGACTATGGTGACAGCTGGAG	317	CAAGAAGCCCTGTGTTCCTG	380
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s22	Exon21	0	AE100p85p86	XPNPEP2_X21.f2a	GAGGCTCCAGACTCTCCTGTT	318	TTAGGAATGATGGGTTCACATG	381
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s23	Exon21	0	AE100p85p86	XPNPEP2_X21.f2a	GAGGCTCCAGACTCTCCTGTT	319	TTAGGAATGATGGGTTCACATG	382
Bradykinin Receptor B1	BDKRB1	AE103s1	Exon2	0	AE103p13p14	U48231_X2.f3a	CACTTTGCAAGGATTGTGGAG	320	AAGAAAGCCAAGCTTCTTGGT	383
Bradykinin Receptor B1	BDKRB1	AE103s2	Exon2	0	AE103p5p6	U48231_X2.f1a	TGGCTCTGTGCCAATAAAACT	321	CACCACCAGGAAGATGCTG	384
Bradykinin Receptor B1	BDKRB1	AE103s3	Exon3	0	AE103p17p18	U48231_X2.f4a	AGGACCAAGGTCTGGGAACT	322	TGGAGGCCAGAAATCCTAAAT	385
Bradykinin Receptor B1	BDKRB1	AE103s4	Exon1	0	AE103p1p2	U48231_X1a	GCTGCCAGGAAGATTAAATGA	323	ATCTCAGTACTTTGGGAGGCC	386
Bradykinin Receptor B1	BDKRB1	AE103s5	Exon3	0	AE103p25p26	U48231_X2.f6a	ACTTCCCAGACTCAAGGGATC	324	CGTGGTGTGTTCATGCAATT	387
Bradykinin Receptor B2	BDKRB2	AE104s1	Intron1	1	AE104p33p34	BDKRB2_X1.f1a	CGACTAGGTCCTCACCAGACA	325	CTCAGTGTCCAGGGAAATGC	388
Bradykinin Receptor B2	BDKRB2	AE104s2	Intron1	1	AE104p33p34	BDKRB2_X1.f1a	CGACTAGGTCCTCACCAGACA	326	CTCAGTGTCCAGGGAAATGC	389
Bradykinin Receptor B2	BDKRB2	AE104s3	Intron1	1	AE104p39p40	BDKRB2_X1.f2	GCAGGCAAATACCACTTTCAA	327	CCGAGGTTCTCTGGAGAAAAA	390
Bradykinin Receptor B2	BDKRB2	AE104s4	Intron1	1	AE104p39p40	BDKRB2_X1.f2	GCAGGCAAATACCACTTTCAA	328	CCGAGGTTCTCTGGAGAAAAA	391
Bradykinin Receptor B2	BDKRB2	AE104s5	Intron1	1	AE104p39p40	BDKRB2_X1.f2	GCAGGCAAATACCACTTTCAA	329	CCGAGGTTCTCTGGAGAAAAA	392
Bradykinin Receptor B2	BDKRB2	AE104s6	Intron1	1	AE104p39p40	BDKRB2_X1.f2	GCAGGCAAATACCACTTTCAA	330	CCGAGGTTCTCTGGAGAAAAA	393
Bradykinin Receptor B2	BDKRB2	AE104s7	Intron2	1	AE104p29p30	BDKRB2_X2a	GCTCTTTCTGGAAGGTCCACT	331	ATACCAACAGCTTCCCCAGTT	394
Bradykinin Receptor B2	BDKRB2	AE104s8	Exon3	1	AE104p25p26	BDKRB2_X3.f7a	GGTCTCAGCACTGTGATCCTC	332	CAAAGACTCAAGTGGGAACGA	395
Bradykinin Receptor B2	BDKRB2	AE104s9	Exon3	1	AE104p25p26	BDKRB2_X3.f7a	GGTCTCAGCACTGTGATCCTC	333	CAAAGACTCAAGTGGGAACGA	396
Bradykinin Receptor B2	BDKRB2	AE104s10	Exon3	1	AE104p25p26	BDKRB2_X3.f7a	GGTCTCAGCACTGTGATCCTC	334	CAAAGACTCAAGTGGGAACGA	397
Bradykinin Receptor B2	BDKRB2	AE104s11	Exon3	1	AE104p9p10	BDKRB2_X3.f3a	TCTACATGCCAGAAGCCTGTT	335	CCACTCTCCTCTGCCTCAGTA	398
Bradykinin Receptor B2	BDKRB2	AE104s12	Exon3	1	AE104p9p10	BDKRB2_X3.f3a	TCTACATGCCAGAAGCCTGTT	336	CCACTCTCCTCTGCCTCAGTA	399
Bradykinin Receptor B2	BDKRB2	AE104s13	Exon3	1	AE104p9p10	BDKRB2_X3.f3a	TCTACATGCCAGAAGCCTGTT	337	CCACTCTCCTCTGCCTCAGTA	400
Bradykinin Receptor B2	BDKRB2	AE104s14	Exon3	1	AE104p21p22	BDKRB2_X3.f6a	CCTCCAGCTTCTAGCTCAGGT	338	GCAGAATCAGTATTGGGAGCC	401
Bradykinin Receptor B2	BDKRB2	AE104s16	3' Flank	1	AE104p3p4	BDKRB2_X3.f1	GCTTAATGCTTGGGTGATGAA	339	CTAGAATCATAGGCGCAGCAG	402
Bradykinin Receptor B2	BDKRB2	AE104s17	3' Flank	1	AE104p3p4	BDKRB2_X3.f1	GCTTAATGCTTGGGTGATGAA	340	CTAGAATCATAGGCGCAGCAG	403
Tachykinin Receptor 1	TACR1	AE106s1	Exon1	1	AE106p23p24	TACR1_X1.f1	CGTGGTCCTCTATGAGCACTT	341	CATCTCCACTAACACCTCGGA	404
Tachykinin Receptor 1	TACR1	AE106s2	Exon2	1	AE106p17p18	TACR1_X2a	GGGTATATGTGAGAAATGCTTGC	342	TCATCAGGAATCAAAGGGTTTC	405
Tachykinin Receptor 1	TACR1	AE106s3	Intron3	1	AE106p13p14	TACR1_X3a	CTGGGTTCCAAAGACACTGAA	343	TATGCAGGTGACAAGTCTCCC	406
Tachykinin Receptor 1	TACR1	AE106s4	Exon5	1	AE106p1p2	TACR1_X5.f1a	CTGCAGGAGGCTAATCTGAGA	344	TCCAACTGCTCTTCACGAAGT	407
Tachykinin Receptor 1	TACR1	AE106s5	Exon5	1	AE106p1p2	TACR1_X5.f1a	CTGCAGGAGGCTAATCTGAGA	345	TCCAACTGCTCTTCACGAAGT	408
Tachykinin Receptor 1	TACR1	AE106s6	Exon5	1	AE106p1p2	TACR1_X5.f1a	CTGCAGGAGGCTAATCTGAGA	346	TCCAACTGCTCTTCACGAAGT	409
Tachykinin Receptor 1	TACR1	AE106s7	Exon5	1	AE106p5p6	TACR1_X5.f2a	ACCCATACTGACCCTTTTTGC	347	TAACAAGCTGATGCAGTGGTG	410
C1 Esterase Inhibitor	C1NH	AE105s1	Intron4	0	AE105p17p18	C1NH_X4a	AATACCCTCCATTCCAGCCT	348	TGGAGTGACCTAATGCTCCTG	411
C1 Esterase Inhibitor	C1NH	AE105s2	Intron6	0	AE105p25p26	C1NH_X6a	GTCTTCCCATTCTGGGTCCT	349	GGTGGAAATACAGATGGAAGGA	412
C1 Esterase Inhibitor	C1NH	AE105s3	Exon7	0	AE105p29p30	C1NH_X7a	CACTGTTCACCCAGCTGGTAT	350	ACATCTTAGGGATCCCCCTTT	413
C1 Esterase Inhibitor	C1NH	AE105s4	Exon3	0	AE105p9p10	C1NH_X3.f1a	AGATTGCTCATCTGCTGCACT	351	AGTAGTGGGCTGGGTAGGAGA	414
C1 Esterase Inhibitor	C1NH	AE105s5	Exon3	0	AE105p13p14	C1NH_X3.f2a	TTCAGCCACCAAAATAACAGC	352	TGGATTGGTGACTCTTATGGG	415
C1 Esterase Inhibitor	C1NH	AE105s6	Exon8	0	AE105p33p34	C1NH_X8.f1a	GAACCCAGAGAATTCAGGACA	353	GTGGATAGCGGACACCTGAG	416
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s1	Exon4	0	AE107p13p14	KLK1_X4a	GACTACAGCCACGACCTCATG	354	GCTCTCAGAAGCCAGTTCAGA	417
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s2	Intron4	0	AE107p13p14	KLK1_X4a	GACTACAGCCACGACCTCATG	355	GCTCTCAGAAGCCAGTTCAGA	418
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s3	Exon3	0	AE107p13p14	KLK1_X4a	GACTACAGCCACGACCTCATG	356	GCTCTCAGAAGCCAGTTCAGA	419
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s4	Intron4	0	AE107p13p14	KLK1_X4a	GACTACAGCCACGACCTCATG	357	GCTCTCAGAAGCCAGTTCAGA	420
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s5	3' Flank	0	AE107p17p18	KLK1_X5a	GCTCCCCAGGCAGAACTT	358	CTGCTGGTGACCTCAGACTTC	421
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s6	3' Flank	0	AE107p17p18	KLK1_X5a	GCTCCCCAGGCAGAACTT	359	CTGCTGGTGACCTCAGACTTC	422

Table VIII (2 of 2)

GENE_DESCRIPTION	HGNC_ID	SNP_ID	EXON	REVCOMP	PCR Amplicon_Name	Target_Name	PCR Left primer	PCR Left primer (SEQ ID NO:)	PCR Right primer	PCR Right primer (SEQ ID NO:)
Bradykinin Receptor B1	BDKRB1	AE103s6	Exon3	0	AE103p9p10	U48231_X2.f2a	GCCTCTGATCTGGTGTTTGTC	707	CTGTGGTCTTGCTATCCTTCG	739
Bradykinin Receptor B1	BDKRB1	AE103s7	Exon3	0	AE103p9p10	U48231_X2.f2a	GCCTCTGATCTGGTGTTTGTC	708	CTGTGGTCTTGCTATCCTTCG	740
Bradykinin Receptor B1	BDKRB1	AE103s8	Exon3	0	AE103p9p10	U48231_X2.f2a	GCCTCTGATCTGGTGTTTGTC	709	CTGTGGTCTTGCTATCCTTCG	741
Bradykinin Receptor B1	BDKRB1	AE103s9	Exon3	0	AE103p13p14	U48231_X2.f3a	CACTTTGCAAGGATTGTGGAG	710	AAGAAAGCCAAGCTTCTTGGT	742
Bradykinin Receptor B2	BDKRB2	AE104s18	Intron1 or Exon	1	AE104p65p66	BDKRB2_X3-5a	GGCAGGGCAGGAATTAGTCT	711	AGATCCAGACAGAGAGGAGGG	743
Bradykinin Receptor B2	BDKRB2	AE104s19	Exon2	1	AE104p65p66	BDKRB2_X3-5a	GGCAGGGCAGGAATTAGTCT	712	AGATCCAGACAGAGAGGAGGG	744
Bradykinin Receptor B2	BDKRB2	AE104s20	5'Flank	1	AE104p89p90	BDKRB2_x1-3a	CTGGGATTTCTTTGTATGCCA	713	AGAGCCTACAGCCAGTTCACA	745
Bradykinin Receptor B2	BDKRB2	AE104s21	5'Flank	1	AE104p89p90	BDKRB2_x1-3a	CTGGGATTTCTTTGTATGCCA	714	AGAGCCTACAGCCAGTTCACA	746
Bradykinin Receptor B2	BDKRB2	AE104s22	5'Flank	1	AE104p87p88	BDKRB2_X1-2	ACCTTCGCTCTCCGCTCT	715	AGAAACCTCCGCCATACATCT	747
Bradykinin Receptor B2	BDKRB2	AE104s23	5'Flank	1	AE104p81p82	BDKRB2_X1-1a	ACGACCACAGGGAAACTTCTC	716	GAGGACGTTTTTGCCGTC	748
Bradykinin Receptor B2	BDKRB2	AE104s24	Exon3	1	AE104p65p66	BDKRB2_X3-5a	GGCAGGGCAGGAATTAGTCT	717	AGATCCAGACAGAGAGGAGGG	749
Bradykinin Receptor B2	BDKRB2	AE104s25	Exon3	1	AE104p65p66	BDKRB2_X3-5a	GGCAGGGCAGGAATTAGTCT	718	AGATCCAGACAGAGAGGAGGG	750
Bradykinin Receptor B2	BDKRB2	AE104s26	Exon3	1	AE104p61p62	BDKRB2_x3-4a	GACCTCCTTGTCCATCAGTGA	719	GGGCTGCTGTGAATTTGTGTA	751
Bradykinin Receptor B2	BDKRB2	AE104s27	Exon3	1	AE104p57p58	BDKRB2_X3-3a	TCCCAGTTACGTCTGCGTAAT	720	GCTGAGTGCACAAGTGAGTTG	752
Bradykinin Receptor B2	BDKRB2	AE104s28	Exon3	1	AE104p53p54	BDKRB2_X3-2a	GCCACCTTCCAATAAACCATT	721	GGGTGATATGGACAGCAGAAG	753
Bradykinin Receptor B2	BDKRB2	AE104s29	Exon3	1	AE104p53p54	BDKRB2_X3-2a	GCCACCTTCCAATAAACCATT	722	GGGTGATATGGACAGCAGAAG	754
Angiotensin Converting Enzyme 2	ACE2	AE109s1	Intron14	1	AE109p25p26	ACE2_x14a	TTAAAAACCCAAAGCCAAAGG	723	TTTCTCGTTTTCCAAAAGCCT	755
Angiotensin Converting Enzyme 2	ACE2	AE109s2	Intron12	1	AE109p29p30	ACE2_x13a	CACCATAGCAGAGAAAGAAGCA	724	GCCAAGTCAAAGAGAAGAAACC	756
Angiotensin Converting Enzyme 2	ACE2	AE109s3	Intron13	1	AE109p29p30	ACE2_x13a	CACCATAGCAGAGAAAGAAGCA	725	GCCAAGTCAAAGAGAAGAAACC	757
Angiotensin Converting Enzyme 2	ACE2	AE109s4	Intron3	1	AE109p69p70	ACE2_x3a	GTAAGGTTGGCAGACATCAGG	726	AAAAATCATGTGGTCAAAAGGA	758
Angiotensin Converting Enzyme 2	ACE2	AE109s5	Intron2	1	AE109p69p70	ACE2_x3a	GTAAGGTTGGCAGACATCAGG	727	AAAAATCATGTGGTCAAAAGGA	759
Angiotensin Converting Enzyme 2	ACE2	AE109s6	Intron16	1	AE109p17p18	ACE2_x16a	CTGTGGGATCCTTCTGGAATT	728	CAATTACATCCTCTCATTGTTTGC	760
Angiotensin Converting Enzyme 2	ACE2	AE109s7	Exon16	1	AE109p17p18	ACE2_x16a	CTGTGGGATCCTTCTGGAATT	729	CAATTACATCCTCTCATTGTTTGC	761
Protease Inhibitor 4	PI4	AE110s1	Intron1	0	AE110p21p22	PI4_X2a	GGACATCTTGATGGGCTCATA	730	TGGGGCACTGTCTTTCATTAG	762
Protease Inhibitor 4	PI4	AE110s2	Exon2	0	AE110p21p22	PI4_X2a	GGACATCTTGATGGGCTCATA	731	TGGGGCACTGTCTTTCATTAG	763
Protease Inhibitor 4	PI4	AE110s3	Intron2	0	AE110p25p26	PI4_X3a	GCCTGGGTACAAAGGAACCT	732	CCGAGTTCTCTAGGGATTGCT	764
Protease Inhibitor 4	PI4	AE110s4	Intron2	0	AE110p25p26	PI4_X3a	GCCTGGGTACAAAGGAACCT	733	CCGAGTTCTCTAGGGATTGCT	765
Protease Inhibitor 4	PI4	AE110s5	Exon1	0	AE110p17p18	PI4_X1.f5a	AAGAACATCTTTTTCTCCCCG	734	CAACAAATTAGTGGGTTGGAGG	766
Protease Inhibitor 4	PI4	AE110s6	5'Flank	0	AE110p5p6	PI4_X1.f2a	TAGAAGCTTTTTGGCCTGACA	735	TGAGCTCTGCACAGCACTAGA	767
Protease Inhibitor 4	PI4	AE110s7	5'Flank	0	AE110p5p6	PI4_X1.f2a	TAGAAGCTTTTTGGCCTGACA	736	TGAGCTCTGCACAGCACTAGA	768
Protease Inhibitor 4	PI4	AE110s8	5'Flank	0	AE110p1p2	PI4_X1.f1a	ATGGTGAGACCCCGACTCTAT	737	TGTTACCCCGTACAGACAAGG	769
Protease Inhibitor 4	PI4	AE110s9	5'Flank	0	AE110p1p2	PI4_X1.f1a	ATGGTGAGACCCCGACTCTAT	738	TGTTACCCCGTACAGACAAGG	770
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s24	Intron11	0	AE100p45p46	XPNPEP2_X12a	TTTTCAAAGCTCCACATCCTG	962	TCGAGTTGTCCTGCTTTCAG	988
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s25	Intron13	0	AE100p49p50	XPNPEP2_X13a	TAAATGACAGGTCAGGGCTTG	963	CAGCTCTCAGGCCTTTTCATT	989
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s26	Intron13	0	AE100p49p50	XPNPEP2_X13a	TAAATGACAGGTCAGGGCTTG	964	CAGCTCTCAGGCCTTTTCATT	990
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s27	Intron7	0	AE100p29p30	XPNPEP2_X8a	GGCCCATGTCATTAATGAGTAC	965	TCAGGGCTACCTTTTGTCCTT	991
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s28	Exon21	0	AE100p93p94	XPNPEP2_X21.f4a	GAACTTTCCAAAGTGCAGCC	966	ACACATACTCTCAAGCCCACG	992
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s29	Exon21	0	AE100p93p94	XPNPEP2_X21.f4a	GAACTTTCCAAAGTGCAGCC	967	ACACATACTCTCAAGCCCACG	993
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s30	Exon6	0	AE100p17p18	XPNPEP2_X5a	GAGAATCTCTTTCCAGAGGCC	968	TGCACGCTCTCACCTATACCT	994
Bradykinin Receptor B1	BDKRB1	AE103s10	Exon3	0	AE103p25p26	U48231_X2.f6a	ACTTCCCAGACTCAAGGGATC	969	CGTGGTGTGTTCATGCAATT	995
Bradykinin Receptor B1	BDKRB1	AE103s11	Exon3	0	AE103p25p26	U48231_X2.f6a	ACTTCCCAGACTCAAGGGATC	970	CGTGGTGTGTTCATGCAATT	996
Bradykinin Receptor B1	BDKRB1	AE103s12	Exon3	0	AE103p25p26	U48231_X2.f6a	ACTTCCCAGACTCAAGGGATC	971	CGTGGTGTGTTCATGCAATT	997
Bradykinin Receptor B1	BDKRB1	AE103s13	Exon3	0	AE103p25p26	U48231_X2.f6a	ACTTCCCAGACTCAAGGGATC	972	CGTGGTGTGTTCATGCAATT	998
Bradykinin Receptor B1	BDKRB1	AE103s14	Exon3	0	AE103p25p26	U48231_X2.f6a	ACTTCCCAGACTCAAGGGATC	973	CGTGGTGTGTTCATGCAATT	999
Bradykinin Receptor B2	BDKRB2	AE104s30	Exon3	1	AE104p53p54	BDKRB2_X3.f2a	GCCACCTTCCAATAAACCATT	974	GGGTGATATGGACAGCAGAAG	1000
Bradykinin Receptor B2	BDKRB2	AE104s31	Exon3	1	AE104p81p82	BDKRB2_X1.f1a	ACGACCACAGGGAAACTTCTC	975	GAGGACGTTTTTGCCGTC	1001
Bradykinin Receptor B2	BDKRB2	AE104s32	Intron1	1	AE104p81p82	BDKRB2_X1.f1a	ACGACCACAGGGAAACTTCTC	976	GAGGACGTTTTTGCCGTC	1002
Bradykinin Receptor B2	BDKRB2	AE104s33	Intron1	1	AE104p81p82	BDKRB2_X1.f1a	ACGACCACAGGGAAACTTCTC	977	GAGGACGTTTTTGCCGTC	1003
Bradykinin Receptor B2	BDKRB2	AE104s34	Exon3	1	AE104p73p74	BDKRB2_X3.f7a	TCGCTGTACTCCTTCATGGTC	978	TTTTTGTCCTTCCCTTGTGAC	1004
Bradykinin Receptor B2	BDKRB2	AE104s35	Exon3	1	AE104p73p74	BDKRB2_X3.f7a	TCGCTGTACTCCTTCATGGTC	979	TTTTTGTCCTTCCCTTGTGAC	1005
Bradykinin Receptor B2	BDKRB2	AE104s36	Exon3	1	AE104p73p74	BDKRB2_X3.f7a	TCGCTGTACTCCTTCATGGTC	980	TTTTTGTCCTTCCCTTGTGAC	1006
Protease Inhibitor 4	PI4	AE110s10	Exon4	0	AE110p29p30	PI4_X4a	ATTTCTGGCTCTCGCAGTCTT	981	CCTTTCCAGAGGCAGAAACTT	1007
Protease Inhibitor 4	PI4	AE110s11	Exon1	0	AE110p1p2	PI4_X1.f1a	ATGGTGAGACCCCGACTCTAT	982	TGTTACCCCGTACAGACAAGG	1008
Protease Inhibitor 4	PI4	AE110s12	5' Flank	0	AE110p1p2	PI4_X1.f1a	ATGGTGAGACCCCGACTCTAT	983	TGTTACCCCGTACAGACAAGG	1009
Tachykinin Receptor 1	TACR1	AE106s8	Intron4	1	AE106p9p10	TACR1_X4a	AAGTTAGCTGCAGTCCCCACT	984	GCTTCATCCCATACTGTGCA	1010
Tachykinin Receptor 1	TACR1	AE106s9	Intron3	1	AE106p13p14	TACR1_X3a	CTGGGTTCCAAAGACACTGAA	985	TATGCAGGTGACAAGTCTCCC	1011
Angiotensin Converting Enzyme 2	ACE2	AE109s8	Intron13	1	AE109p29p30	ACE2_X13a	CACCATAGCAGAGAAAGAAGCA	986	GCCAAGTCAAAGAGAAGAAACC	1012
Angiotensin Converting Enzyme 2	ACE2	AE109s9	Intron6	1	AE109p57p58	ACE2_X6a	CAAAATGCGATTTCTACAATGTT	987	TGGAATGGAAATTAGAATTGGTT	1013

Table IX (1 of 2)

TARGET SEQUENCE

GENE_DESCRIPTION	HGNC_ID	SNP_ID	EXON	REVCOMP	Target_Name	Forward sequencing primer	forward seq name	Forward sequencing primer (SEQ ID NO:)	Reverse sequencing primer	reverse seq name	Reverse sequencing primer (SEQ ID NO:)
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s1	Exon20	0	XPNPEP2_X20a	AGTTCGTCCTCCTCCCTCACT	AE100p79	423	AGGCTGGTCTGACTGGAAAGT	AE100p80	486
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s2	Intron3	0	XPNPEP2_X3a	CAGTAACATCAGTTGCCACCC	AE100p11	424	TCCTGTTTGTGGTCTCTGACC	AE100p12	487
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s3	Intron15	0	XPNPEP2_X15a	CACTTGTGGAAAGCACACAGA	AE100p59	425	TGTCAGTGGCCTGAAATATCC	AE100p60	488
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s4	Intron15	0	XPNPEP2_X15a	CACTTGTGGAAAGCACACAGA	AE100p59	426	TGTCAGTGGCCTGAAATATCC	AE100p60	489
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s5	Intron1	0	XPNPEP2_X1a	CCTCTGTCTCTGAGATCTTTGGA	AE100p3	427	AGAGGTCAGAGCTGCCTTCC	AE100p4	490
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s6	Intron7	0	XPNPEP2_X7a	GCAAAGGGAACCAGGACTAAC	AE100p27	428	TAAACAAGCATCCCAGGTGAC	AE100p28	491
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s7	Intron7	0	XPNPEP2_X7a	GCAAAGGGAACCAGGACTAAC	AE100p27	429	TAAACAAGCATCCCAGGTGAC	AE100p28	492
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s8	Intron10	0	XPNPEP2_X10a	CTTTGCATCCTTAGCAGATGC	AE100p39	430	AAGAAGGGAACTCAGTGCACA	AE100p40	493
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s9	Intron10	0	XPNPEP2_X10a	CTTTGCATCCTTAGCAGATGC	AE100p39	431	AAGAAGGGAACTCAGTGCACA	AE100p40	494
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s10	Intron7	0	XPNPEP2_X7a	GCAAAGGGAACCAGGACTAAC	AE100p27	432	TAAACAAGCATCCCAGGTGAC	AE100p28	495
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s11	Intron13	0	XPNPEP2_X13a	AGTTGAGAGGTAGAGGCAGCC	AE100p51	433	GCAACTCCCTACTCCACACTG	AE100p52	496
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s12	Intron13	0	XPNPEP2_X13a	AGTTGAGAGGTAGAGGCAGCC	AE100p51	434	GCAACTCCCTACTCCACACTG	AE100p52	497
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s13	Intron13	0	XPNPEP2_X13a	AGTTGAGAGGTAGAGGCAGCC	AE100p51	435	GCAACTCCCTACTCCACACTG	AE100p52	498
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s14	Exon1	0	XPNPEP2_X1a	CCTCTGTCTCTGAGATCTTTGGA	AE100p3	436	AGAGGTCAGAGCTGCCTTCC	AE100p4	499
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s15	Exon1	0	XPNPEP2_X1a	CCTCTGTCTCTGAGATCTTTGGA	AE100p3	437	AGAGGTCAGAGCTGCCTTCC	AE100p4	500
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s16	Intron8	0	XPNPEP2_X8a	AGGGTTTCGCTGCTTTTTAAG	AE100p31	438	CTTACCCTTCTTGGTTCCCAC	AE100p32	501
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s17	Intron17	0	XPNPEP2_X17a	CAAGGTGGACAGTCTTCGGTA	AE100p67	439	AGCTGGGTAACCTTGGGTAGA	AE100p68	502
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s18	Intron17	0	XPNPEP2_X17a	CAAGGTGGACAGTCTTCGGTA	AE100p67	440	AGCTGGGTAACCTTGGGTAGA	AE100p68	503
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s19	Intron15	0	XPNPEP2_X15a	CACTTGTGGAAAGCACACAGA	AE100p59	441	TGTCAGTGGCCTGAAATATCC	AE100p60	504
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s20	Intron21	0	XPNPEP2_X21.f1a	CAAGACTTCACCTCTTGGCAG	AE100p83	442	TGGGACCTTCTCCATAGGTCT	AE100p84	505
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s21	Exon21	0	XPNPEP2_X21.f1a	CAAGACTTCACCTCTTGGCAG	AE100p83	443	TGGGACCTTCTCCATAGGTCT	AE100p84	506
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s22	Exon21	0	XPNPEP2_X21.f2a	ACTGAACATACCCCAAGAGCC	AE100p87	444	GGTTGATGTTTCATGCCCTG	AE100p88	507
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s23	Exon21	0	XPNPEP2_X21.f2a	ACTGAACATACCCCAAGAGCC	AE100p87	445	GGTTGATGTTTCATGCCCTG	AE100p88	508
Bradykinin Receptor B1	BDKRB1	AE103s1	Exon2	0	U48231_X2 f3a	TCTGGGTTTCCTCCTACCACT	AE103p15	446	TCAATGCTGTTTTAATTCCGC	AE103p16	509
Bradykinin Receptor B1	BDKRB1	AE103s2	Exon2	0	U48231_X2.f1a	GACAGGTTGGTTTGGCTCATA	AE103p7	447	ATGAACAAATTGGCCTTGATG	AE103p8	510
Bradykinin Receptor B1	BDKRB1	AE103s3	Exon3	0	U48231_X2.f4a	CACCCCTAAAAGTCTTGCTCC	AE103p19	448	AGGACCCATTCCTTCTGGAG	AE103p20	511
Bradykinin Receptor B1	BDKRB1	AE103s4	Exon1	0	U48231_X1a	GCCTGGAACACAGACCATTAA	AE103p3	449	GGATCAGATGAACCCAGGAGT	AE103p4	512
Bradykinin Receptor B1	BDKRB1	AE103s5	Exon3	0	U48231_X2 f6a	CTCAGCCTCCTGTAGCTGAGA	AE103p27	450	TGGTGTGTTCATGCAATTTCT	AE103p28	513
Bradykinin Receptor B2	BDKRB2	AE104s1	Intron1	1	BDKRB2_X1 f1a	GCACCGAGAGCAATAAATGTC	AE104p35	451	CTTTGGGATTCCCTCCCTT	AE104p36	514
Bradykinin Receptor B2	BDKRB2	AE104s2	Intron1	1	BDKRB2_X1.f1a	GCACCGAGAGCAATAAATGTC	AE104p35	452	CTTTGGGATTCCCTCCCTT	AE104p36	515
Bradykinin Receptor B2	BDKRB2	AE104s3	Intron1	1	BDKRB2_X1 f2	GCAGGCAAATACCACTTTCAA	AE104p39	453	CCGAGGTTCTCTGGAGAAAAA	AE104p40	516
Bradykinin Receptor B2	BDKRB2	AE104s4	Intron1	1	BDKRB2_X1 f2	GCAGGCAAATACCACTTTCAA	AE104p39	454	CCGAGGTTCTCTGGAGAAAAA	AE104p40	517
Bradykinin Receptor B2	BDKRB2	AE104s5	Intron1	1	BDKRB2_X1.f2	GCAGGCAAATACCACTTTCAA	AE104p39	455	CCGAGGTTCTCTGGAGAAAAA	AE104p40	518
Bradykinin Receptor B2	BDKRB2	AE104s6	Intron1	1	BDKRB2_X1.f2	GCAGGCAAATACCACTTTCAA	AE104p39	456	CCGAGGTTCTCTGGAGAAAAA	AE104p40	519
Bradykinin Receptor B2	BDKRB2	AE104s7	Intron2	1	BDKRB2_X2a	GAGCTGAACTACGAGTCACGG	AE104p31	457	GGTCCACTTGTCCTCCTTCTT	AE104p32	520
Bradykinin Receptor B2	BDKRB2	AE104s8	Exon3	1	BDKRB2_X3 f7a	ATCTTCCTCTGCCTCATCACA	AE104p27	458	CAGAAAGCTGTTCGACGAGAC	AE104p28	521
Bradykinin Receptor B2	BDKRB2	AE104s9	Exon3	1	BDKRB2_X3 f7a	ATCTTCCTCTGCCTCATCACA	AE104p27	459	CAGAAAGCTGTTCGACGAGAC	AE104p28	522
Bradykinin Receptor B2	BDKRB2	AE104s10	Exon3	1	BDKRB2_X3 f7a	ATCTTCCTCTGCCTCATCACA	AE104p27	460	CAGAAAGCTGTTCGACGAGAC	AE104p28	523
Bradykinin Receptor B2	BDKRB2	AE104s11	Exon3	1	BDKRB2_X3 f3a	AAAGGCTTCTGAGTGTGCAAG	AE104p11	461	TGGAGGAAGAAAACAGGTGAA	AE104p12	524
Bradykinin Receptor B2	BDKRB2	AE104s12	Exon3	1	BDKRB2_X3 f3a	AAAGGCTTCTGAGTGTGCAAG	AE104p11	462	TGGAGGAAGAAAACAGGTGAA	AE104p12	525
Bradykinin Receptor B2	BDKRB2	AE104s13	Exon3	1	BDKRB2_X3 f3a	AAAGGCTTCTGAGTGTGCAAG	AE104p11	463	TGGAGGAAGAAAACAGGTGAA	AE104p12	526
Bradykinin Receptor B2	BDKRB2	AE104s14	Exon3	1	BDKRB2_X3 f6a	CAGGTTCTAGCCCTTCTTGGT	AE104p23	464	ACACAGTAGGTGCTCATTGGC	AE104p24	527
Bradykinin Receptor B2	BDKRB2	AE104s16	3' Flank	1	BDKRB2_X3 f1	TGGGAGTATGAAACAAGTGGC	AE104p5	465	TGGATGAGGTTTTTGCATAGC	AE104p6	528
Bradykinin Receptor B2	BDKRB2	AE104s17	3' Flank	1	BDKRB2_X3 f1	TGGGAGTATGAAACAAGTGGC	AE104p5	466	TGGATGAGGTTTTTGCATAGC	AE104p6	529
Tachykinin Receptor 1	TACR1	AE108s1	Exon1	1	TACR1_X1.f1	TTGTGGGCTAAGATGATCCAC	AE108p25	467	TTACCGCAAGAGAGATGCTGT	AE108p26	530
Tachykinin Receptor 1	TACR1	AE108s2	Exon2	1	TACR1_X2a	GAAAGAAAGAGCAAGAAGGGG	AE108p19	468	TGGCAGGAAAAATATGGAATC	AE108p20	531
Tachykinin Receptor 1	TACR1	AE108s3	Intron3	1	TACR1_X3a	CCTCTCCTCCTCTCTGTTGCT	AE108p15	469	GTAGCTGCCAAACCTTGACTG	AE108p16	532
Tachykinin Receptor 1	TACR1	AE108s4	Exon5	1	TACR1_X5.f1a	GGCTCCAGGAAAATGAGTCTT	AE108p3	470	GAGAGCTTCAGCTTCTCCTCC	AE108p4	533
Tachykinin Receptor 1	TACR1	AE108s5	Exon5	1	TACR1_X5.f1a	GGCTCCAGGAAAATGAGTCTT	AE108p3	471	GAGAGCTTCAGCTTCTCCTCC	AE108p4	534
Tachykinin Receptor 1	TACR1	AE108s6	Exon5	1	TACR1_X5.f1a	GGCTCCAGGAAAATGAGTCTT	AE108p3	472	GAGAGCTTCAGCTTCTCCTCC	AE108p4	535
Tachykinin Receptor 1	TACR1	AE108s7	Exon5	1	TACR1_X5 f2a	ATGGTTCCAGATGAAGGGAAT	AE108p7	473	AGGGTCACCTGTTCATCTGCT	AE108p8	536
C1 Esterase Inhibitor	C1NH	AE105s1	Intron4	0	C1NH_X4a	CCGACTCATCCTGCAAGTATC	AE105p19	474	TCTGCAGTCCATCCCTGATAC	AE105p20	537
C1 Esterase Inhibitor	C1NH	AE105s2	Intron6	0	C1NH_X6a	CCCCAAGTTCTACAATCGGAT	AE105p27	475	ACCCCAAAATGATGGGACTAC	AE105p28	538
C1 Esterase Inhibitor	C1NH	AE105s3	Exon7	0	C1NH_X7a	AAGCCTGGAAGCTTAGGTCTG	AE105p31	476	CCTGGGAGTAACCCTAAGCTG	AE105p32	539
C1 Esterase Inhibitor	C1NH	AE105s4	Exon3	0	C1NH_X3.f1a	TTTCCACATCCACACCTTCTC	AE105p11	477	ATCTGTTGGGAGCTGGGTAGT	AE105p12	540
C1 Esterase Inhibitor	C1NH	AE105s5	Exon3	0	C1NH_X3 f2a	ATACCACTGATGAACCCACCA	AE105p15	478	GTCCAACAAATGACCTGGAGA	AE105p16	541
C1 Esterase Inhibitor	C1NH	AE105s6	Exon8	0	C1NH_X8.f1a	CTCCATCAGCTGAGGGTATCA	AE105p35	479	GAGCTGAGGCTGGAGAGGTAG	AE105p36	542
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s1	Exon4	0	KLK1_X4a	CCTGACAGAGCCTGCTGATAC	AE107p15	480	CCTCACCACACAGGTGTCTTT	AE107p16	543
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s2	Intron4	0	KLK1_X4a	CCTGACAGAGCCTGCTGATAC	AE107p15	481	CCTCACCACACAGGTGTCTTT	AE107p16	544
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s3	Exon3	0	KLK1_X4a	CCTGACAGAGCCTGCTGATAC	AE107p15	482	CCTCACCACACAGGTGTCTTT	AE107p16	545
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s4	Intron4	0	KLK1_X4a	CCTGACAGAGCCTGCTGATAC	AE107p15	483	CCTCACCACACAGGTGTCTTT	AE107p16	546
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s5	3' Flank	0	KLK1_X5a	CCCCGTAGACCTTTCTCACTC	AE107p19	484	GTGCACCACATCTGGAAAGAT	AE107p20	547
Kallikrein 1 (renal/pancreas/salivary)	KLK1	AE107s6	3' Flank	0	KLK1_X5a	CCCCGTAGACCTTTCTCACTC	AE107p19	485	GTGCACCACATCTGGAAAGAT	AE107p20	548
Bradykinin Receptor B1	BDKRB1	AE103s6	Exon3	0	U48231_X2.f2a	CCCTTCTGGGCAGAGAATATC	AE103p11	771	CACTCTTGTCCTGCTGACCTC	AE103p12	803
Bradykinin Receptor B1	BDKRB1	AE103s7	Exon3	0	U48231_X2.f2a	CCCTTCTGGGCAGAGAATATC	AE103p11	772	CACTCTTGTCCTGCTGACCTC	AE103p12	804
Bradykinin Receptor B1	BDKRB1	AE103s8	Exon3	0	U48231_X2.f2a	CCCTTCTGGGCAGAGAATATC	AE103p11	773	CACTCTTGTCCTGCTGACCTC	AE103p12	805
Bradykinin Receptor B1	BDKRB1	AE103s9	Exon3	0	U48231_X2.f3a	TCTGGGTTTCCTCCTACCACT	AE103p15	774	TCAATGCTGTTTTAATTCCGC	AE103p16	806
Bradykinin Receptor B2	BDKRB2	AE104s18	Iron1 or Exo	1	BDKRB2_X3-5a	GGTGTTTTACCGGAGACATCA	AE104p67	775	GGTTGTGCTGCTGCTATTCAT	AE104p68	807
Bradykinin Receptor B2	BDKRB2	AE104s19	Exon2	1	BDKRB2_X3-5a	GGTGTTTTACCGGAGACATCA	AE104p67	776	GGTTGTGCTGCTGCTATTCAT	AE104p68	808
Bradykinin Receptor B2	BDKRB2	AE104s20	5'Flank	1	BDKRB2_x1-3a	CAGAAGCTGTCCTGTTTCCTG	AE104p91	777	GCCACCCATAAACTGATCTGA	AE104p92	809
Bradykinin Receptor B2	BDKRB2	AE104s21	5'Flank	1	BDKRB2_x1-3a	CAGAAGCTGTCCTGTTTCCTG	AE104p91	778	GCCACCCATAAACTGATCTGA	AE104p92	810
Bradykinin Receptor B2	BDKRB2	AE104s22	5'Flank	1	BDKRB2_X1-2	ACCTTCGCTCTCCGCTCT	AE104p87	779	AGAAACCTCCGCCATACATCT	AE104p88	811
Bradykinin Receptor B2	BDKRB2	AE104s23	5'Flank	1	BDKRB2_X1-1a	CTCTGTGCTGGGACAGTTTGT	AE104p83	780	GAGCTACGCAAACATGGAAAT	AE104p84	812
Bradykinin Receptor B2	BDKRB2	AE104s24	Exon3	1	BDKRB2_X3-5a	GGTGTTTTACCGGAGACATCA	AE104p67	781	GGTTGTGCTGCTGCTATTCAT	AE104p68	813
Bradykinin Receptor B2	BDKRB2	AE104s25	Exon3	1	BDKRB2_X3-5a	GGTGTTTTACCGGAGACATCA	AE104p67	782	GGTTGTGCTGCTGCTATTCAT	AE104p68	814
Bradykinin Receptor B2	BDKRB2	AE104s26	Exon3	1	BDKRB2_x3-4a	AATCCTGGTCTCCAGGTTGTT	AE104p63	783	TGAGGGACAGTTGCTTTTCAG	AE104p64	815
Bradykinin Receptor B2	BDKRB2	AE104s27	Exon3	1	BDKRB2_X3-3a	ACGTAGCACCCTTTGCTTTTC	AE104p59	784	TGCCCTGGGTTTCTTTAATCT	AE104p60	816

Table IX (2 of 2)

GENE_DESCRIPTION	HGNC_ID	SNP_ID	EXON	REVCOMP	Target_Name	Forward sequencing primer	forward seq name	Forward sequencing primer (SEQ ID NO:)	Reverse sequencing primer	reverse seq name	Reverse sequencing primer (SEQ ID NO:)
Bradykinin Receptor B2	BDKRB2	AE104s28	Exon3	1	BDKRB2_X3-2a	TTGCTGAGACAGGAACAGTCC	AE104p55	785	TATTGCACAACCATCTGTCCC	AE104p56	817
Bradykinin Receptor B2	BDKRB2	AE104s29	Exon3	1	BDKRB2_X3-2a	TTGCTGAGACAGGAACAGTCC	AE104p55	786	TATTGCACAACCATCTGTCCC	AE104p56	818
Angiotensin Converting Enzyme 2	ACE2	AE109s1	Intron14	1	ACE2_x14a	TTTTGAAAAGAACCACATGGC	AE109p27	787	AGTGGGATCTTTGGAGGAAAA	AE109p28	819
Angiotensin Converting Enzyme 2	ACE2	AE109s2	Intron12	1	ACE2_x13a	CAGCTGTGTCACAAGTCCTCA	AE109p31	788	ACATCTGGAACCCCTCAAAAG	AE109p32	820
Angiotensin Converting Enzyme 2	ACE2	AE109s3	Intron13	1	ACE2_x13a	CAGCTGTGTCACAAGTCCTCA	AE109p31	789	ACATCTGGAACCCCTCAAAAG	AE109p32	821
Angiotensin Converting Enzyme 2	ACE2	AE109s4	Intron3	1	ACE2_x3a	TCATTCATGTCCTTGCCCTTA	AE109p71	790	TCTTCAGCAAAATTTCCATTGTT	AE109p72	822
Angiotensin Converting Enzyme 2	ACE2	AE109s5	Intron2	1	ACE2_x3a	TCATTCATGTCCTTGCCCTTA	AE109p71	791	TCTTCAGCAAAATTTCCATTGTT	AE109p72	823
Angiotensin Converting Enzyme 2	ACE2	AE109s6	Intron16	1	ACE2_x16a	GCACACAGGAAGAACACACAA	AE109p19	792	CCTCCCCCATGTCTCTCTATC	AE109p20	824
Angiotensin Converting Enzyme 2	ACE2	AE109s7	Exon16	1	ACE2_x16a	GCACACAGGAAGAACACACAA	AE109p19	793	CCTCCCCCATGTCTCTCTATC	AE109p20	825
Protease Inhibitor 4	PI4	AE110s1	Intron1	0	PI4_X2a	GATCTGGAGCGACTGTTTCTG	AE110p23	794	CACACTGATTACCTCTTCCGC	AE110p24	826
Protease Inhibitor 4	PI4	AE110s2	Exon2	0	PI4_X2a	GATCTGGAGCGACTGTTTCTG	AE110p23	795	CACACTGATTACCTCTTCCGC	AE110p24	827
Protease Inhibitor 4	PI4	AE110s3	Intron2	0	PI4_X3a	CTTTCAACATCCATTTGTGGG	AE110p27	796	ACTTTGGATGCCTCCAGTTTT	AE110p28	828
Protease Inhibitor 4	PI4	AE110s4	Intron2	0	PI4_X3a	CTTTCAACATCCATTTGTGGG	AE110p27	797	ACTTTGGATGCCTCCAGTTTT	AE110p28	829
Protease Inhibitor 4	PI4	AE110s5	Exon1	0	PI4_X1 f5a	CTACGCCATGCTTTCCCTG	AE110p19	798	CGGTGGTGTGGATTTAGCATA	AE110p20	830
Protease Inhibitor 4	PI4	AE110s6	5'Flank	0	PI4_X1 f2a	TTGGGGGAGAAACTGGAGTAT	AE110p7	799	CCAACAGAGCAGGAAATGAAG	AE110p8	831
Protease Inhibitor 4	PI4	AE110s7	5'Flank	0	PI4_X1.f2a	TTGGGGGAGAAACTGGAGTAT	AE110p7	800	CCAACAGAGCAGGAAATGAAG	AE110p8	832
Protease Inhibitor 4	PI4	AE110s8	5'Flank	0	PI4_X1.f1a	AAAAATTAGCTGGGTGTGGCT	AE110p3	801	TAAGTGACCTGCCCAAAGTTG	AE110p4	833
Protease Inhibitor 4	PI4	AE110s9	5'Flank	0	PI4_X1 f1a	AAAAATTAGCTGGGTGTGGCT	AE110p3	802	TAAGTGACCTGCCCAAAGTTG	AE110p4	834
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s24	Intron11	0	XPNPEP2_X12a	ATCTCCATCATCTTGGAGCCT	AE100p47	1014	ACCCAAGAACCTGTCACTCCT	AE100p48	1040
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s25	Intron13	0	XPNPEP2_X13a	AGTTGAGAGGTAGAGGCAGCC	AE100p51	1015	GCAACTCCCTACTCCACACTG	AE100p52	1041
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s26	Intron13	0	XPNPEP2_X13a	AGTTGAGAGGTAGAGGCAGCC	AE100p51	1016	GCAACTCCCTACTCCACACTG	AE100p52	1042
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s27	Intron7	0	XPNPEP2_X8a	AGGGTTTCGCTGCTTTTTAAG	AE100p91	1017	CTTACCCTTCTTGGTTCCCAC	AE100p92	1043
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s28	Exon21	0	XPNPEP2_X21 f4a	CAATGCTGTTAAATCCTCCCA	AE100p95	1018	CTCACCCTCTCTTCTTCCTCC	AE100p96	1044
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s29	Exon21	0	XPNPEP2_X21.f4a	CAATGCTGTTAAATCCTCCCA	AE100p95	1019	CTCACCCTCTCTTCTTCCTCC	AE100p96	1045
Aminopeptidase P (membrane-bound)	XPNPEP2	AE100s30	Exon6	0	XPNPEP2_X5a	ACATCCATCAGCTAATGCCAC	AE100p19	1020	GAACCTAGTCCAGGTCCCAAG	AE100p20	1046
Bradykinin Receptor B1	BDKRB1	AE103s10	Exon3	0	U48231_X2 f6a	CTCAGCCTCCTGTAGCTGAGA	AE103p27	1021	TGGTGTGTTCATGCAATTTCT	AE103p28	1047
Bradykinin Receptor B1	BDKRB1	AE103s11	Exon3	0	U48231_X2.f6a	CTCAGCCTCCTGTAGCTGAGA	AE103p27	1022	TGGTGTGTTCATGCAATTTCT	AE103p28	1048
Bradykinin Receptor B1	BDKRB1	AE103s12	Exon3	0	U48231_X2 f6a	CTCAGCCTCCTGTAGCTGAGA	AE103p27	1023	TGGTGTGTTCATGCAATTTCT	AE103p28	1049
Bradykinin Receptor B1	BDKRB1	AE103s13	Exon3	0	U48231_X2 f6a	CTCAGCCTCCTGTAGCTGAGA	AE103p27	1024	TGGTGTGTTCATGCAATTTCT	AE103p28	1050
Bradykinin Receptor B1	BDKRB1	AE103s14	Exon3	0	U48231_X2.f6a	CTCAGCCTCCTGTAGCTGAGA	AE103p27	1025	TGGTGTGTTCATGCAATTTCT	AE103p28	1051
Bradykinin Receptor B2	BDKRB2	AE104s30	Exon3	1	BDKRB2_X3.f2a	TTGCTGAGACAGGAACAGTCC	AE104p55	1026	TATTGCACAACCATCTGTCCC	AE104p56	1052
Bradykinin Receptor B2	BDKRB2	AE104s31	Exon3	1	BDKRB2_X1.f1a	CTCTGTGCTGGGACAGTTTGT	AE104p83	1027	GAGCTACGCAAACATGGAAAT	AE104p84	1053
Bradykinin Receptor B2	BDKRB2	AE104s32	Intron1	1	BDKRB2_X1.f1a	CTCTGTGCTGGGACAGTTTGT	AE104p83	1028	GAGCTACGCAAACATGGAAAT	AE104p84	1054
Bradykinin Receptor B2	BDKRB2	AE104s33	Intron1	1	BDKRB2_X1.f1a	CTCTGTGCTGGGACAGTTTGT	AE104p83	1029	GAGCTACGCAAACATGGAAAT	AE104p84	1055
Bradykinin Receptor B2	BDKRB2	AE104s34	Exon3	1	BDKRB2_X3 f7a	CCCAGATCACCAAGCTGTAGA	AE104p75	1030	CTTTTCCACTTTCTTTCAGCG	AE104p76	1056
Bradykinin Receptor B2	BDKRB2	AE104s35	Exon3	1	BDKRB2_X3 f7a	CCCAGATCACCAAGCTGTAGA	AE104p75	1031	CTTTTCCACTTTCTTTCAGCG	AE104p76	1057
Bradykinin Receptor B2	BDKRB2	AE104s36	Exon3	1	BDKRB2_X3 f7a	CCCAGATCACCAAGCTGTAGA	AE104p75	1032	CTTTTCCACTTTCTTTCAGCG	AE104p76	1058
Protease Inhibitor 4	PI4	AE110s10	Exon4	0	PI4_X4a	TCTCTTGCTGGCTTGGAGATA	AE110p31	1033	CAGGGTGTGGAATGTCCAG	AE110p32	1059
Protease Inhibitor 4	PI4	AE110s11	Exon1	0	PI4_X1.f1a	AAAAATTAGCTGGGTGTGGCT	AE110p3	1034	TAAGTGACCTGCCCAAAGTTG	AE110p4	1060
Protease Inhibitor 4	PI4	AE110s12	5' Flank	0	PI4_X1.f1a	AAAAATTAGCTGGGTGTGGCT	AE110p3	1035	TAAGTGACCTGCCCAAAGTTG	AE110p4	1061
Tachykinin Receptor 1	TACR1	AE106s8	Intron4	1	TACR1_X4a	TGTCCCTCTTGTCTCACAGCT	AE106p11	1036	CTCACCTGTCTCACCCTCTTG	AE106p12	1062
Tachykinin Receptor 1	TACR1	AE106s9	Intron3	1	TACR1_X3a	CCTCTCCTCCTCTCTGTTGCT	AE106p15	1037	GTAGCTGCCAAACCTTGACTG	AE106p16	1063
Angiotensin Converting Enzyme 2	ACE2	AE109s8	Intron13	1	ACE2_X13a	CAGCTGTGTCACAAGTCCTCA	AE109p31	1038	ACATCTGGAACCCCTCAAAAG	AE109p32	1064
Angiotensin Converting Enzyme 2	ACE2	AE109s9	Intron6	1	ACE2_X6a	TAAGGCTCACTCAAAAAGGCA	AE109p59	1039	TCTTCCTGGGCTTTTCAGATT	AE109p60	1065

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SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:)	ORCHID_SNPIT	ORCHID_SNPIT (SEQ ID NO:)
AE100s1	TATCATTTGTGCCCTATGACCG	1066	CAGGGTCAGGGAGAAGGC	1154	CCTCATCGATGTCNGCCTGCTGTCTCC	1242
AE100s10	AAACTTCATCATCAGAGGTACCAAAG	1067	GAGGACATTTTGATTCAGACTCCTC	1155	GTGGTTTGCAAACCTTAGCATGCAC	1243
AE100s11	ATAGAATGACTTCCTCCAGAGGGA	1068	CAGCCTAACCCTGYACTGGG	1156	TGGAAGCCCAGNCCCCAGAGGT	1244
AE100s12	TCCAGAGGGACTGGCCTG	1069	GAAGGGCAGCCTAACCCTG	1157	AGCCCAGGCCCCAGAGGTYCTCCCA	1245
AE100s13	ATAGAATGACTTCCTCCAGAGGGA	1070	GCTGAGAAGGGGAGAGAATGTT	1158	AATGTTGAGAANGNCAGCCTAACCCTG	1246
AE100s14	N/A	N/A	N/A	N/A	N/A	N/A
AE100s15	ACCCTCTGTCTGCTCGAG	1071	GATGGAGGGACAAGGGAG	1159	CCCGGGSCTCTTCCTTCANGCNTTTCCT	1247
AE100s16	AAAGAAGGAAGGAAGGAAAGGAA	1072	GTGTAGGAATAGAAGAAGGGGTTATAGG	1160	AGAAAAGCTTGNCTCAGGCAGATCAGC	1248
AE100s17	N/A	N/A	N/A	N/A	N/A	N/A
AE100s18	AACACAGCAAGACCCCTCTCA	1073	GATCCCAGAGCATCTCTATGAGC	1161	TACCTAAATAAATAATAAAAGCCAG	1249
AE100s19	N/A	N/A	N/A	N/A	N/A	N/A
AE100s2	ATAGAATTTGCAGGGCAGGG	1074	GTATCTTTTGCAGTTCAACTCCCC	1162	GCAACAAGTCTCCTTTNCAGAACAGTC	1250
AE100s20	TACCACAACAGGGGACTGG	1075	GATTCAGGTACTGGAGCTGCG	1163	AGACTTCACCTCTTGGCANCTTGGCTT	1251
AE100s21	N/A	N/A	N/A	N/A	N/A	N/A
AE100s22	N/A	N/A	N/A	N/A	N/A	N/A
AE100s23	TTTGCCTAAGGACACACAAATTT	1076	GAGGTGGGCTCAGGGACT	1164	CTGCATGTTGCTGAAGGGTGAAAGA	1252
AE100s24	CGCTATCTGATCTCCATCATCT	1077	CCGCACCTGGAGTTGGGG	1165	TTNGAGCCTGTGGCTNCAACCAGACCT	1253
AE100s25	N/A	N/A	N/A	N/A	N/A	N/A
AE100s26	N/A	N/A	N/A	N/A	N/A	N/A
AE100s27	ACAAGTAAGAGTTTGTTTGAGGAAAGG	1078	GAGCCCCAAAAAAGTGTAAGTGA	1166	TTACCCTANGGCTGACCTNCCAGGAAC	1254
AE100s28	N/A	N/A	N/A	N/A	N/A	N/A
AE100s29	N/A	N/A	N/A	N/A	N/A	N/A
AE100s3	N/A	N/A	N/A	N/A	N/A	N/A
AE100s30	TATCTTTCTTTCAGTTGGCACCA	1079	CAATGGACAAGAGGAAGGGG	1167	TCACCTGGCTCCTCACCGAGATTCC	1255
AE100s4	TCCCTGCTGCTTCCCCGG	1080	AATATTTGTGCACTGATTTACCAGAATAG	1168	TATTTCAGNCCACTGACANGGCCTCAG	1256
AE100s5	N/A	N/A	N/A	N/A	N/A	N/A
AE100s6	TGTGTGTGCATGAGTGTAGGTG	1081	CTTTGTCATTTCCATACCTGTGAAA	1169	ACCTTCATAGAGGGTATAATAAAAG	1257
AE100s7	ATCCAGTAATGGCAAAGCCAG	1082	GTCAGCCTTAGGGTAACAGTTTTG	1170	AAGAGTTTGTTTGAGGAAAGGGTTT	1258
AE100s8	GCAAATCTCACGTCTGCTG	1083	CAGGTCTGGGGGCACAGTA	1171	GTAAAGGAGGTCTCNATNGCACAGGGG	1259
AE100s9	AAAACTAGGAAAGACAGAAAGCACAC	1084	TTTCAGAGGACTGGCAGGAG	1172	CACAGAGTAGAGAGNATTGCCACGAAA	1260
AE103s1	AACTTCTTTGCCTTCACTAACAGCT	1085	GATGAAGATATTGGAGCAAGACTTTTAG	1173	CCAGTAATTTATGTCTTTGTGGGCC	1261
AE103s10	N/A	N/A	N/A	N/A	N/A	N/A
AE103s11	TGGACTTGATGAATGTTACCAAATT	1086	GACTCTGAGCCTCCTGCCTC	1174	ATCCTGAATTATCCAAGTGGGCCCT	1262
AE103s12	N/A	N/A	N/A	N/A	N/A	N/A
AE103s13	CCACCGAGTTTCTGGTAATTTG	1087	CTTTGAATAGACAAATGGAAGTGTARTAAGA	1175	CAGCAGGAAACAAATAACAAGTATC	1263
AE103s14	TGTCATAGCAGCAGCAGGAA	1088	CCTGGCAGTTAGCCTAGAAAGC	1176	ACAAGTATCRGGTAATGNCCTCTCTTA	1264
AE103s2	TGACAATGCTCCAGAAGCC	1089	CAACAGGACAAAAAGGTTCCC	1177	CTGGGACCTGCTGNACAGAGTGCTGCC	1265
AE103s3	ACTTTTCTGGCGGAATTAAAACA	1090	ACCCCCCAATCTACGGGA	1178	TGAACCAANANGCTTGGCTTTCTTATC	1266
AE103s4	N/A	N/A	N/A	N/A	N/A	N/A
AE103s5	N/A	N/A	N/A	N/A	N/A	N/A
AE103s6	TTCTGGGCAGAGAATATCTGGA	1091	CCACCAGGAAGATGCTGATG	1179	GAGCCCTCCTCTGCCGTGTCATCAA	1267
AE103s7	N/A	N/A	N/A	N/A	N/A	N/A
AE103s8	ATCTGAACATCACCGCCT	1092	GTAGTTGAAGAAGACGATCGC	1180	AGATCTGAACATCACCGCCTGCATC	1268
AE103s9	N/A	N/A	N/A	N/A	N/A	N/A
AE104s1	GAGAGCAATAAATGTCTGTTTTTTGATAA	1093	CTCACCTGTGCTGCTTGTG	1181	CACTGGGCAAATCNGCNGGGCTCCCCC	1269
AE104s10	GGTTGGGGCCTCAGGGTG	1094	GTGGCGGTGTGAAGCACC	1182	GTNGGAATGACAGGTNGAAGGGAGCCA	1270

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SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:)	ORCHID_SNPIT	ORCHID_SNPIT (SEQ ID NO:)
AE104s11	TTGGATGTGAAATGCTTCCTG	1095	GCCCTATGCATGGTGTAGATG	1183	TTACAACATAACAGCNCATTGAGTCTT	1271
AE104s12	ATTTTCTCGTTTGGATGTGAAATG	1096	CGGCCCTATGCATGGTGTA	1184	TAACAGCTCATTGAGTCTTKCACAG	1272
AE104s13	GCCATTGCGGCAGAGCTC	1097	AAAAAAAGAGGCTGTGTTTTGTCA	1185	GGGCAGTCATTCAGCACCAGAGCAC	1273
AE104s14	AAGTGAATGAGTGCTGCCCT	1098	AAGGTGGCCCAGTATGAGC	1186	CCCTAGAAGAGTGTGAAAAGGAATG	1274
AE104s16	GATGCATGGATGGAGGAGG	1099	CAGTGATGGGGAATTCATTATCC	1187	ATTCCTTCACTCATNTATNAAACAAAA	1275
AE104s17	GATGGAACAGATGAAGGAGAGG	1100	CATAAATGCCCCTCCTCCAT	1188	TACGTTGAGCGATGAGCCCCAGGTT	1276
AE104s18	AGAAGAAAAGATGGTTAGATGGCA	1101	CATTGAGTCAGGGACTCAGCA	1189	ACAGGGGCTGGGGATNGCNAAATACAC	1277
AE104s19	TAACTAGTGAACTGAGGAATCCCTTT	1102	CACTCTGAGTCCAAATGTTCTCTC	1190	GTGGTGGGCACGGAGTCCTCAC	1278
AE104s2	GAGAGCAATAAATGTCTGTTTTTTGATAA	1103	CTCACCTGTGCTGCTTGTG	1191	GTCAGGGAGGGGCNCACCTGGGCGCGG	1279
AE104s20	TTTACACTCCCAGGGCTGAG	1104	CTCTTCCCCAGATCCACTGG	1192	TTTTTGNAGCCTTAAAACCCTTCCTTC	1280
AE104s21	GGATTTCTTTGTAYGCCACGTAC	1105	CATACATCTCCGAAGAAACGG	1193	GCAGAAGCTGTCCTGTTTCCTGGGT	1281
AE104s22	N/A	N/A	N/A	N/A	N/A	N/A
AE104s23	AGAGCTGGAGTGGCGGCG	1106	GCAGGAGTGCAGAGCTCAG	1194	GAAGTGCCCAGGAGGCTGNTGACATCA	1282
AE104s24	N/A	N/A	N/A	N/A	N/A	N/A
AE104s25	N/A	N/A	N/A	N/A	N/A	N/A
AE104s26	TGAATAGATTAAAGAAACCCAGGG	1107	GTTCTCCGTCCCTGCCCC	1195	CATTGCACCAAANCTGGATGGC	1283
AE104s27	TCGACCGTCTCGTCGAAC	1108	GAAAGAGAAGGAGCCATCTCCA	1196	GCTTTCNGGTGGTGNCAGTGCCCAGTC	1284
AE104s28	N/A	N/A	N/A	N/A	N/A	N/A
AE104s29	N/A	N/A	N/A	N/A	N/A	N/A
AE104s3	TTTGCAAGGGAGGGAATC	1109	CAACCCTGCACTCCAAGC	1197	GAGCGAAGGGCTGGCTGAGGTCATG	1285
AE104s30	N/A	N/A	N/A	N/A	N/A	N/A
AE104s31	N/A	N/A	N/A	N/A	N/A	N/A
AE104s32	N/A	N/A	N/A	N/A	N/A	N/A
AE104s33	TAGGGATACAATGGCTAGGAGCT	1110	GTTTGGGACCCCATGTTCTAT	1198	ACCTTTTGCTTGATTTTTCACTGTA	1286
AE104s34	ACACTGGTGCTTCACACCG	1111	GTACATGTGAGGCATCWTTACGC	1199	GGCTCCCAATACTGATTCTGCTCCA	1287
AE104s35	N/A	N/A	N/A	N/A	N/A	N/A
AE104s36	CCCTTCTGCTGTCCATATCA	1112	CATCTTGAAGGAACTCAAAGACTCA	1200	ACCCACAGCACCCTGCTNGACCGTCTC	1288
AE104s4	AGTGAGAGGCTTGGAGTGCA	1113	CTTTGGATGAAAAAGAGGAAGCA	1201	AGGGTTGCAGGGAGANCTGGGATGAGG	1289
AE104s5	TGCAGGGTTGCAGGGAGA	1114	CAAGAGAAGGCGTCTTTGGAT	1202	GCTGGGATGANGYCTGGGGTGCTGCCT	1290
AE104s6	GGCTCACAACTGTGGAATGTC	1115	CAAAGAGGCCCTGCCCGA	1203	GTTCTCTGGAGAAAAAACTGTGCTG	1291
AE104s7	AACTGTGGCCCAGAGGGT	1116	AACCCCTTACCCACCAGC	1204	CCCCCTCTCCAAGTCTNTGTCCCACAA	1292
AE104s8	ATGTACGTAGCACCCTTTGCTTT	1117	GGAGACCAAGGTTCCAGCTC	1205	GAAGAGGGAACTGAGGCAGGGACAG	1293
AE104s9	TATTTCTAGACCTCAGTGTCTTTTCCTTATAG	1118	GAAGTCGTTGTGAGGGTTAAAGG	1206	AAGGGTGCTACGTANATNTGAGGCATC	1294
AE105s1	GAGAGGACTCTGAAGGGGG	1119	AGGTCTTCACCTGCTCTGCA	1207	CCCAGCGCTGGGGAAAGAAAGGACA	1295
AE105s2	ATTGTGACAGAGGGTGGGG	1120	CAAACTCAGATTGTGGGAGAGC	1208	GAGATGCGGTAGGAAGACTGTTAAG	1296
AE105s3	N/A	N/A	N/A	N/A	N/A	N/A
AE105s4	GCGAAGGGAAGGTCGCAA	1121	TTGAGTTGGTTGTCGGCAA	1209	AAGCTGGAANCCTCNAGGATGGGTTCA	1297
AE105s5	TGTTGGGGGATGCTTTGG	1122	GATGCTGAATGGGGAAAAGG	1210	AAGCTCTACCACGCCTTCTCAG	1298
AE105s6	ATCTCTGTGGCCCGCACC	1123	CATATACTCGCCCCATGAAGAC	1211	GGAACTTGTNCTNCTGGTCCCAGAGCA	1299
AE106s1	TATCAAAGGCCACAGCCG	1124	CACAACGAATGGTACTACGGC	1212	TACTGGCGAAGACAGCGGCGATGGG	1300
AE106s2	ATGGTCTCTGTGGTTGAGTAGTAGC	1125	CATCATACATCCCCTCCAGC	1213	CCAGCAGGAGAGCCAGGACCCA	1301
AE106s3	ATACCTGGGGATATTTTGTGC	1126	CTACCACGAGCAAGTCTCTG	1214	CCAAGCGCAAGGTGAGCAGGGG	1302
AE106s4	TGCAGAATTCATCCTGAAATGA	1127	CTGTKTGACTCAAACCAAATCACT	1215	AGGTCGGACCANCTTTTCCCAA	1303
AE106s5	AAAAGCTGGTCCGACCTTTTATT	1128	TCAAAAAATCTCAATTCTTCCCTATCT	1216	TCCCTATCTTTGCNACNCTNATGCTGT	1304
AE106s6	TTTGAGTCAMACAGCATGAGG	1129	CATGGAAATTCCCTTCATCTG	1217	ACCCATACTGACCCTTTTNGCAAGTCC	1305
AE106s7	ATGGTCTTGGAGTCACTTCGTG	1130	CCCACGAGGAGGAGCCAG	1218	AGAGCAGTTNGAGGTCAGGTNCAGGGA	1306

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SNP_ID	ORCHID_LEFT	ORCHID_LEFT (SEQ ID NO:)	ORCHID_RIGHT	ORCHID_RIGHT (SEQ ID NO:)	ORCHID_SNPIT	ORCHID_SNPIT (SEQ ID NO:)
AE106s8	N/A	N/A	N/A	N/A	N/A	N/A
AE106s9	N/A	N/A	N/A	N/A	N/A	N/A
AE107s1	GTTCGTAGTCTCATTTCCAGATGATC	1131	ACACACAGCATGAAGTCTGTCAC	1219	CAAAATCCTGCCTAATGATGAGTGC	1307
AE107s2	AGCATCGAACCAGAGAATTGTATG	1132	CTTCCCTGGCCCTTTCTC	1220	TCCCTTGNACRCAGGAGTCCCCATCCC	1308
AE107s3	CCTGCTGATACCATCACAGATG	1133	CATACAATTCTCTGGTTCGATGC	1221	GCTGTGAAGNTCGNGGAGTTGCCCACC	1309
AE107s4	ATCGAACCAGAGAATTGTATGTGG	1134	GGGAGAAAAAGGGCTGCA	1222	AAGGCRGGGATGGGGACTCCTG	1310
AE107s5	ACCTGGACCCACTCGGCT	1135	CCTTTCCCCACCTGCTGG	1223	TGNGGCCACCCCAGCTGTGTCA	1311
AE107s6	CCAGTAAAATCAAATGTGCATCC	1136	CAGCCTCAGCCGAGTGGG	1224	ATGTGTGTCACGTTCTGCCATCACC	1312
AE109s1	AATAGCTTATCCAATAAGGAATAGGTTACTTT	1137	GAATTGATTATTTTTGAGTGCACAGTC	1225	ATCTGGAACTTATAGTNTTGAAAAGAA	1313
AE109s2	GGGGGTTCAGGGCCTTTT	1138	GCAAATTTAGCCAAGTCAAAGAGA	1226	GAGGGGTTCCAGANGTACNTATATTTA	1314
AE109s3	TGGGGCCAAAGGAGACTAG	1139	GCTGAAAGACCAGAACAAGAATTC	1227	AAGTAGACAAGGAATGGGTGTGAAA	1315
AE109s4	GTGTTGAAACACACATATCTGCAAT	1140	TGGAAAAGTTTGTAACCCAGATAATC	1228	TCATAATCACNANTNAAANTTAGTAGC	1316
AE109s5	GTGTTCAACTGCAAATTAAAGATAATAAACA	1141	ACATGGCAAAGAAGTAAATTGCTG	1229	GAAATTTTGCTGAAGAGAATGCTAA	1317
AE109s6	AACTCAAATCAAGATTATTCCCCTG	1142	GTTACCAAATACAACAACAATAACCAGTATT	1230	CACATGTAAATGACTCAGAATAATG	1318
AE109s7	CCCTCACCCTTAGATGAAAGTAAAA	1143	TTTGAAACCAAGAATCTCCTTTAATTT	1231	TTCAGTTCTAGGAATNATATCAGACAC	1319
AE109s8	N/A	N/A	N/A	N/A	N/A	N/A
AE109s9	AGGCTCACTCAAAAAGGCAATT	1144	TGCCTCCCTGCTCATTTG	1232	CTTGGTAANAAGCCCCATNAATTCTTC	1320
AE110s1	N/A	N/A	N/A	N/A	N/A	N/A
AE110s10	CACCTTGGACGTGGATGAG	1145	ATGTGGCGATTGGTCTGG	1233	GGNTGGCACCGAGGNTGCAGCAGCCAC	1321
AE110s11	CACCTCCTGCACACTCTCA	1146	CATGGTGTCATTCAGGAATTTTG	1234	AACCTCNCCGGNCATGGGCTGGAAACA	1322
AE110s12	AGATTTGGGGGAGAAACTGG	1147	CAGTAGAACTGGTCTTTGTATTGTTACC	1235	TNTCTTGGACAGATGTTNATTATGAAA	1323
AE110s2	CTGTACCTTCTTTTCATCTTCCCTT	1148	GCAGCATCATGGGCACCC	1236	CCGGACTGNTGTGTTCTCATCAACATA	1324
AE110s3	AAGGAGGGCTCTGCCCAG	1149	GATGCAACTCTAGCTTCTTGTAAAAATT	1237	GATCCTGGCTTGTTCANTANTCTAATG	1325
AE110s4	N/A	N/A	N/A	N/A	N/A	N/A
AE110s5	CTTATCAACGACCACGTCAAGAA	1150	GATTTAGCATATACCAATGATCTGACTCT	1238	GAGGGAAGATTGTGGATTTGGTCAG	1326
AE110s6	GTCAAACTAAATGGCTGAAAGTGG	1151	TTTCAGATGAGTTGATTTCATTAGTGC	1239	AGACCCTAAAATAAACTCTGAGGAT	1327
AE110s7	AGGGTCAAACTAAATGGCTGAAA	1152	CACTTGTCTTTCAGATGAGTTGATTTC	1240	TAAACCATATAAAGCACTCCACAGA	1328
AE110s8	AGAAACTGGAGTATCCTTTCTTGGA	1153	CTGTAGAGGTCAGTAGAACTGGTCTTTG	1241	TATGAAACGNGTACCANTTCTATCCCC	1329
AE110s9	N/A	N/A	N/A	N/A	N/A	N/A

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SNP_ID	GBS_LEFT	GBS_LEFT (SEQ ID NO:)	GBS_RIGHT	GBS_RIGHT (SEQ ID NO:)
AE100s1	TGTAAAACGACGGCCAGTAGTTCCTCCTCCTCCCTCACT	1330	CAGGAAACAGCTATGACCAGAAGCTCTGGGGTCTC	1451
AE100s10	TGTAAAACGACGGCCAGTGGCATTCACAGGTGATTCAGT	1331	CAGGAAACAGCTATGACCCACCAGGCAAGCAAATC	1452
AE100s11	TGTAAAACGACGGCCAGTTTCTGGGCTTTACCCTCTCTC	1332	CAGGAAACAGCTATGACCAGGTCTGAGCAGAGACA	1453
AE100s12	TGTAAAACGACGGCCAGTTTCTGGGCTTTACCCTCTCTC	1333	CAGGAAACAGCTATGACCAGGTCTGAGCAGAGACA	1454
AE100s13	TGTAAAACGACGGCCAGTCCAGGTGCAGGATTAACAGAC	1334	CAGGAAACAGCTATGACCAGGTCTGAGCAGAGACA	1455
AE100s14	TGTAAAACGACGGCCAGTACTAGGAACTTGCACAGTCCG	1335	CAGGAAACAGCTATGACCATGCACATACCACAGAG	1456
AE100s15	TGTAAAACGACGGCCAGTCCTCACACCCTATCCTACACG	1336	CAGGAAACAGCTATGACCATGCACATACCACAGAG	1457
AE100s16	TGTAAAACGACGGCCAGTCAGTGAGATCTTGCCACTGC	1337	CAGGAAACAGCTATGACCCAAGCTAAGGAAAAGCC	1458
AE100s17	TGTAAAACGACGGCCAGTCAGGCAGACAATGATGTGATG	1338	CAGGAAACAGCTATGACCTGTGCTCCTCTGAAGTC	1459
AE100s18	TGTAAAACGACGGCCAGTTATCCAGGTATGGTGGCATGT	1339	CAGGAAACAGCTATGACCATAGCGATGTTGTTGGA	1460
AE100s19	TGTAAAACGACGGCCAGTCAGAGGGAAGCACGTGATG	1340	CAGGAAACAGCTATGACCACTGGTTTCTGAAACCC	1461
AE100s2	TGTAAAACGACGGCCAGTTGTAAAGCCCTTTGCAGAAGT	1341	CAGGAAACAGCTATGACCCTTGTCAGCTACAAGCC	1462
AE100s20	TGTAAAACGACGGCCAGTCTCTGAAAAGCCCCAGAGAAT	1342	CAGGAAACAGCTATGACCCTGTTGAAGCCACTCGA	1463
AE100s21	TGTAAAACGACGGCCAGTGAGGCTCCAGACTCTCCTGTT	1343	CAGGAAACAGCTATGACCGGAGCAGCTGTAGCAGT	1464
AE100s22	TGTAAAACGACGGCCAGTCATTGCCTAGAAACCTTTGCA	1344	CAGGAAACAGCTATGACCATTGCTCTCTTGGGGTT	1465
AE100s23	TGTAAAACGACGGCCAGTAGCCACAGCTACAATGCTGTT	1345	CAGGAAACAGCTATGACCAAAACCCAGAGGCAAGT	1466
AE100s24	TGTAAAACGACGGCCAGTCTGCCGTCAACACAGAACTCT	1346	CAGGAAACAGCTATGACCGAACTTGTCCACGATCT	1467
AE100s25	TGTAAAACGACGGCCAGTAGAAGAACAGTTCTCCTCCGG	1347	CAGGAAACAGCTATGACCCCATGTGAACTCGTGAG	1468
AE100s26	TGTAAAACGACGGCCAGTCATGCCTTGCCTTGTACTTTC	1348	CAGGAAACAGCTATGACCGGCAACTCCCTACTCCA	1469
AE100s27	TGTAAAACGACGGCCAGTATGGAACACAGAGGGGTTAGG	1349	CAGGAAACAGCTATGACCGTCTGCAAATCCACACT	1470
AE100s28	TGTAAAACGACGGCCAGTGGGTTGTATACCACACCCTGG	1350	CAGGAAACAGCTATGACCACAGCCAAATTCCTATG	1471
AE100s29	TGTAAAACGACGGCCAGTCGAGATAGGAAAGCCAGCTAG	1351	CAGGAAACAGCTATGACCGTTCTCCAACCTCTGGT	1472
AE100s3	TGTAAAACGACGGCCAGTCACTTGTGGAAAGCACACAGA	1352	CAGGAAACAGCTATGACCTGTCAGTGGCCTGAAAT	1473
AE100s30	TGTAAAACGACGGCCAGTAGGAAATTTGAGGCCATCACT	1353	CAGGAAACAGCTATGACCCCTCCTTCTACCAAGGT	1474
AE100s4	TGTAAAACGACGGCCAGTAGCAGTCAAGATCCCTTCCAT	1354	CAGGAAACAGCTATGACCGTTTCCTGAACACCTCT	1475
AE100s5	TGTAAAACGACGGCCAGTGAAAGAGCCCTCCCTCTCTC	1355	CAGGAAACAGCTATGACCTTGCAATGCGGTAGTCT	1476
AE100s6	TGTAAAACGACGGCCAGTCAAGGTGGACAGTCTTCGGTA	1356	CAGGAAACAGCTATGACCCTGCTGGCATTCCTCAC	1477
AE100s7	TGTAAAACGACGGCCAGTTCCTCATAGCAGCCCTATTGA	1357	CAGGAAACAGCTATGACCGGACGCCAGATACTTTC	1478
AE100s8	TGTAAAACGACGGCCAGTATCCGAAGACAGGGAGTTCAT	1358	CAGGAAACAGCTATGACCCTGTTCTTCACTGCCTT	1479
AE100s9	TGTAAAACGACGGCCAGTATCCGAAGACAGGGAGTTCAT	1359	CAGGAAACAGCTATGACCTGGGGAGTAGGTGTCTG	1480
AE103s1	TGTAAAACGACGGCCAGTTCTTTGCCTTCCTGGAATTCT	1360	CAGGAAACAGCTATGACCTCAATGCTGTTTTAATT	1481
AE103s10	TGTAAAACGACGGCCAGTCGTCCCAGATCTGAACATCAC	1361	CAGGAAACAGCTATGACCGACTGCTTGCACCTGGA	1482
AE103s11	TGTAAAACGACGGCCAGTGAACCAAGAAGCTTGGCTTTC	1362	CAGGAAACAGCTATGACCCTAAATCTGTTTCCCTG	1483
AE103s12	TGTAAAACGACGGCCAGTAACTTCCCAGACTCAAGGGAT	1363	CAGGAAACAGCTATGACCTCCCTGTATTCCTGGCA	1484
AE103s13	TGTAAAACGACGGCCAGTCAAGTGATCCTCCACTTTGGT	1364	CAGGAAACAGCTATGACCTGGTGTGTTCATGCAAT	1485
AE103s14	TGTAAAACGACGGCCAGTCCTCCACTTTGGTCTCCCATA	1365	CAGGAAACAGCTATGACCTGGTGTGTTCATGCAAT	1486
AE103s2	TGTAAAACGACGGCCAGTGCTGTAGTCTGCCACTTCCTG	1366	CAGGAAACAGCTATGACCGATATTCTCTGCCCAGA	1487
AE103s3	TGTAAAACGACGGCCAGTAGGACCAAGGTCTGGGAACT	1367	CAGGAAACAGCTATGACCCTGAATTCCTCTGGCCT	1488
AE103s4	TGTAAAACGACGGCCAGTGCCTGGAACACAGACCATTAA	1368	CAGGAAACAGCTATGACCAAGGCAGATGGATCAGA	1489
AE103s5	TGTAAAACGACGGCCAGTAACTTCCCAGACTCAAGGGAT	1369	CAGGAAACAGCTATGACCTCCCTGTATTCCTGGCA	1490
AE103s6	TGTAAAACGACGGCCAGTCCCTTCTGGGCAGAGAATATC	1370	CAGGAAACAGCTATGACCAGTGGTAGGAGGAAACC	1491
AE103s7	TGTAAAACGACGGCCAGTCCCTTCTGGGCAGAGAATATC	1371	CAGGAAACAGCTATGACCAGTGGTAGGAGGAAACC	1492
AE103s8	TGTAAAACGACGGCCAGTGCATCTTCCTGGTGGTGG	1372	CAGGAAACAGCTATGACCCTGTGGTCTTGCTATCC	1493
AE103s9	TGTAAAACGACGGCCAGTCGTCCCAGATCTGAACATCAC	1373	CAGGAAACAGCTATGACCAGAATTCCAGGAAGGCA	1494
AE104s1	TGTAAAACGACGGCCAGTGTGGTCTTTAAAGGAGGCCTG	1374	CAGGAAACAGCTATGACCGACTTTTGCACCAACCG	1495
AE104s10	TGTAAAACGACGGCCAGTGGTCTCAGCACTGTGATCCTC	1375	CAGGAAACAGCTATGACCGTGCTACGTACATGTGA	1496

AE104s11	TGTAAAACGACGGCCAGTTCGGGAGTTGTAACAAATGCT	1376	CAGGAAACAGCTATGACCGAGGCTGTGTTTTGTCA	1497
AE104s12	TGTAAAACGACGGCCAGTGCTATGCAAAAACCTCATCCA	1377	CAGGAAACAGCTATGACCGAGGCTGTGTTTTGTCA	1498
AE104s13	TGTAAAACGACGGCCAGTCATCTACACCATGCATAGGGC	1378	CAGGAAACAGCTATGACCTGGAGGAAGAAAACAGG	1499
AE104s14	TGTAAAACGACGGCCAGTTAGCCTCTCCAGTTCTAGCCC	1379	CAGGAAACAGCTATGACCATTTCTAATCGGTCTTG	1500
AE104s16	TGTAAAACGACGGCCAGTAATAAAAGAGGTGCTGACCCAC	1380	CAGGAAACAGCTATGACCCTAGAATCATAGGCGCA	1501
AE104s17	TGTAAAACGACGGCCAGTCCACCATGACCCAAGTTTAT	1381	CAGGAAACAGCTATGACCGCCACTTGTTTCATACT	1502
AE104s18	TGTAAAACGACGGCCAGTGAGGAATCCCTTTGACTCACC	1382	CAGGAAACAGCTATGACCGACTGAGCAATGTCTGG	1503
AE104s19	TGTAAAACGACGGCCAGTTGGTTCCTTCAACTGTTGTCC	1383	CAGGAAACAGCTATGACCACAAACGTCCATTGAGT	1504
AE104s2	TGTAAAACGACGGCCAGTGTGGTCTTTAAAGGAGGCCTG	1384	CAGGAAACAGCTATGACCGACTTTTGCACCAACCG	1505
AE104s20	TGTAAAACGACGGCCAGTAGATGTATGGCGGAGGTTTCT	1385	CAGGAAACAGCTATGACCGCCACCCATAAACTGAT	1506
AE104s21	TGTAAAACGACGGCCAGTTTTTGGATGTAAACAGTGGGC	1386	CAGGAAACAGCTATGACCAATGTTTTGAAAGTCCC	1507
AE104s22	TGTAAAACGACGGCCAGTGGAAGCCCCATGTGAATAAAT	1387	CAGGAAACAGCTATGACCTTGAGCAAAACTGAGAA	1508
AE104s23	TGTAAAACGACGGCCAGTACTTCAGTCGCTCCCTGGTAC	1388	CAGGAAACAGCTATGACCACATGGAAATCTTCGCA	1509
AE104s24	TGTAAAACGACGGCCAGTTCTCCATCTGAATGGGTTCTG	1389	CAGGAAACAGCTATGACCACGAGATGCAGAAGTTC	1510
AE104s25	TGTAAAACGACGGCCAGTAAGCAACTGTCCCTCAATCCT	1390	CAGGAAACAGCTATGACCTAATCACACAGATCGCC	1511
AE104s26	TGTAAAACGACGGCCAGTGACCTCCTTGTCCATCAGTGA	1391	CAGGAAACAGCTATGACCCCAAGGACTCCAAAATC	1512
AE104s27	TGTAAAACGACGGCCAGTCCCTCACAACGACTTCATGTT	1392	CAGGAAACAGCTATGACCTCACTGATGGACAAGGA	1513
AE104s28	TGTAAAACGACGGCCAGTTTCTCTCCAAATGCTCCTGTG	1393	CAGGAAACAGCTATGACCGGGTGATATGGACAGCA	1514
AE104s29	TGTAAAACGACGGCCAGTGGTCTCAGCACTGTGATCCTC	1394	CAGGAAACAGCTATGACCGTGCTACGTACATGTGA	1515
AE104s3	TGTAAAACGACGGCCAGTGCAGGCAAATACCACTTTCAA	1395	CAGGAAACAGCTATGACCTTGGATGAAAAAGAGGA	1516
AE104s30	TGTAAAACGACGGCCAGTCCCAATACTGATTCTGCTCCA	1396	CAGGAAACAGCTATGACCGGAACTCAAAGACTCAA	1517
AE104s31	TGTAAAACGACGGCCAGTTGGTTCCTTCAACTGTTGTCC	1397	CAGGAAACAGCTATGACCTTGAGTCAGGGACTCAG	1518
AE104s32	TGTAAAACGACGGCCAGTCCTGACTCAATGGACGTTTGT	1398	CAGGAAACAGCTATGACCAATCCATATTCACACCA	1519
AE104s33	TGTAAAACGACGGCCAGTCCTGACTCAATGGACGTTTGT	1399	CAGGAAACAGCTATGACCAATCCATATTCACACCA	1520
AE104s34	TGTAAAACGACGGCCAGTATCTTCCTCTGCCTCATCACA	1400	CAGGAAACAGCTATGACCTATTGCACAACCATCTG	1521
AE104s35	TGTAAAACGACGGCCAGTTCAGACTTTGAAGACATGGCC	1401	CAGGAAACAGCTATGACCTATTGCACAACCATCTG	1522
AE104s36	TGTAAAACGACGGCCAGTTGTACGTAGCACCCTTTGCTT	1402	CAGGAAACAGCTATGACCTCACTGATGGACAAGGA	1523
AE104s4	TGTAAAACGACGGCCAGTGAATCCCAAAGAGATTGAGGC	1403	CAGGAAACAGCTATGACCACAAGCTTGGAGGAAGC	1524
AE104s5	TGTAAAACGACGGCCAGTGAATCCCAAAGAGATTGAGGC	1404	CAGGAAACAGCTATGACCGACATTCCACAGTTGTG	1525
AE104s6	TGTAAAACGACGGCCAGTTGCTTCCTCTTTTTCATCCAA	1405	CAGGAAACAGCTATGACCCAGCCTACAGGAAGTGG	1526
AE104s7	TGTAAAACGACGGCCAGTGGACCCACAAATCAATGCTT	1406	CAGGAAACAGCTATGACCATACCAACAGCTTCCCC	1527
AE104s8	TGTAAAACGACGGCCAGTTGCTCCACGGAGCTATTTCTA	1407	CAGGAAACAGCTATGACCCAAAGACTCAAGTGGGA	1528
AE104s9	TGTAAAACGACGGCCAGTGTGGGAATGACAGGTGGAAG	1408	CAGGAAACAGCTATGACCGGGTGATATGGACAGCA	1529
AE105s1	TGTAAAACGACGGCCAGTAGAGCATCCTCTCTTACCCCA	1409	CAGGAAACAGCTATGACCACTGTACCTGCCCGGTT	1530
AE105s2	TGTAAAACGACGGCCAGTAAGCCTGGAAGCTTAGGTCTG	1410	CAGGAAACAGCTATGACCTTTGATGCGGGGTAGTG	1531
AE105s3	TGTAAAACGACGGCCAGTTATTTTCTAGGTGGGGCAGCT	1411	CAGGAAACAGCTATGACCTACCCCTCTAACTTGCA	1532
AE105s4	TGTAAAACGACGGCCAGTGAACCACAGGATAGAGCCTCC	1412	CAGGAAACAGCTATGACCATCTGTTGGGAGCTGGG	1533
AE105s5	TGTAAAACGACGGCCAGTACTACCCAGCTCCCAACAGAT	1413	CAGGAAACAGCTATGACCTGGATTGGTGACTCTTA	1534
AE105s6	TGTAAAACGACGGCCAGTGGACCCAGATCTTCAGGTTTC	1414	CAGGAAACAGCTATGACCAACTGAGAGCTGAGGCT	1535
AE106s1	TGTAAAACGACGGCCAGTAGAGTGGCCAATCTTCCACTT	1415	CAGGAAACAGCTATGACCGTGGATCATCTTAGCCC	1536
AE106s2	TGTAAAACGACGGCCAGTGGCATGGGGAGTCATCTCTAC	1416	CAGGAAACAGCTATGACCTGGCAGGAAAAATATGG	1537
AE106s3	TGTAAAACGACGGCCAGTCAGATCTGGGTTCCAAAGACA	1417	CAGGAAACAGCTATGACCCTGATCTACTTCCTCCC	1538
AE106s4	TGTAAAACGACGGCCAGTCTTTTGTTCACCCTGTCAAGC	1418	CAGGAAACAGCTATGACCTTGCAAAAAGGGTCAGT	1539
AE106s5	TGTAAAACGACGGCCAGTGGCTCCAGGAAAATGAGTCTT	1419	CAGGAAACAGCTATGACCTCTGGAACCATCAGAAA	1540
AE106s6	TGTAAAACGACGGCCAGTAAAAGCTGGTCCGACCTTTTA	1420	CAGGAAACAGCTATGACCTCCAACTGCTCTTCACG	1541
AE106s7	TGTAAAACGACGGCCAGTTGAGGGTGTTTCTGATGGTTC	1421	CAGGAAACAGCTATGACCATGAAATCCACCCGGTA	1542
AE106s8	TGTAAAACGACGGCCAGTATGGATTTCTGGTTCCCTTTG	1422	CAGGAAACAGCTATGACCCTTCTTCCTCCTGCCCT	1543
AE106s9	TGTAAAACGACGGCCAGTCTTTAAGAGCAAGCGAAGTGG	1423	CAGGAAACAGCTATGACCCACACTATGGGCCAGTG	1544
AE107s1	TGTAAAACGACGGCCAGTAATTGTATGTGGGGGCAGACT	1424	CAGGAAACAGCTATGACCGTGAAGCAGATGCCTGG	1545

AE107s2	TGTAAAACGACGGCCAGTCCTGACAGAGCCTGCTGATAC	1425	CAGGAAACAGCTATGACCATTTTGAGGTCCACACA	1546
AE107s3	TGTAAAACGACGGCCAGTGCCCAGTTTGTTCATGTCAGT	1426	CAGGAAACAGCTATGACCGGAAATGAGACTACGAA	1547
AE107s4	TGTAAAACGACGGCCAGTCCTGACAGAGCCTGCTGATAC	1427	CAGGAAACAGCTATGACCAAGTCTGTCACCTTCTG	1548
AE107s5	TGTAAAACGACGGCCAGTCCCTACCCCCAGTAAAATCAA	1428	CAGGAAACAGCTATGACCACCTCTCAGCCTCAGAC	1549
AE107s6	TGTAAAACGACGGCCAGTGCCGTCAGAGTGCTGTCTTAT	1429	CAGGAAACAGCTATGACCCTGTTTGTCTGCACCTG	1550
AE109s1	TGTAAAACGACGGCCAGTTGACGAGAGTCAATTGAAAGGA	1430	CAGGAAACAGCTATGACCATGCAGACCAAAGCATC	1551
AE109s2	TGTAAAACGACGGCCAGTCAAAGTAGTTGAGCAGTGGCC	1431	CAGGAAACAGCTATGACCGACCATACAACAATTGG	1552
AE109s3	TGTAAAACGACGGCCAGTAAATGGCAGCTGTCACCATAG	1432	CAGGAAACAGCTATGACCACATGAATGTAAGGCCA	1553
AE109s4	TGTAAAACGACGGCCAGTTCTGCAGAGAAAATAAACCACTGA	1433	CAGGAAACAGCTATGACCTCTTCAGCAAAATTTCC	1554
AE109s5	TGTAAAACGACGGCCAGTGCATTCTTGTGGATTATCTGGG	1434	CAGGAAACAGCTATGACCTCGACAGTGGGGAAACT	1555
AE109s6	TGTAAAACGACGGCCAGTTTGCCCATAGTGGTAACTTGC	1435	CAGGAAACAGCTATGACCCGAGTGGCTAATTTGAA	1556
AE109s7	TGTAAAACGACGGCCAGTGCACACAGGAAGAACACACAA	1436	CAGGAAACAGCTATGACCCTCCCCCATGTCTCTCT	1557
AE109s8	TGTAAAACGACGGCCAGTGTGCATGCATCTGTGTGTGTT	1437	CAGGAAACAGCTATGACCACATGAATGTAAGGCCA	1558
AE109s9	TGTAAAACGACGGCCAGTTGCTTTCAAAATGCGATTTCT	1438	CAGGAAACAGCTATGACCCTTTCTTCCTGGGCTTT	1559
AE110s1	TGTAAAACGACGGCCAGTCAGGCATGTCAGGTTTTGAAT	1439	CAGGAAACAGCTATGACCTTGTAATCCATCCGTAG	1560
AE110s10	TGTAAAACGACGGCCAGTCTTGCTGTGTTATCCCCAAGA	1440	CAGGAAACAGCTATGACCCTCCTGCTTGGAACAGA	1561
AE110s11	TGTAAAACGACGGCCAGTAAGAACATCTTTTTCTCCCCG	1441	CAGGAAACAGCTATGACCATCCACAATCTTCCCTC	1562
AE110s12	TGTAAAACGACGGCCAGTGCAGGTCATGGAAGTGGATTA	1442	CAGGAAACAGCTATGACCAGCCATTTAGTTTGACC	1563
AE110s2	TGTAAAACGACGGCCAGTGATCTGGAGCGACTGTTTCTG	1443	CAGGAAACAGCTATGACCTTTGCCTTGGTTAGGGA	1564
AE110s3	TGTAAAACGACGGCCAGTCTTTCAACATCCATTTGTGGG	1444	CAGGAAACAGCTATGACCTGACGACTTACTTTGGA	1565
AE110s4	TGTAAAACGACGGCCAGTCACAGGAAGCAACCTCTGAAG	1445	CAGGAAACAGCTATGACCGGAGCCAGAAATGGAGA	1566
AE110s5	TGTAAAACGACGGCCAGTCCTTGCAAAATTCCTGAATGA	1446	CAGGAAACAGCTATGACCAGGGTTGCTCAACCCTA	1567
AE110s6	TGTAAAACGACGGCCAGTCCTTGTCTGTACGGGGTAACA	1447	CAGGAAACAGCTATGACCCCAACAGAGCAGGAAAT	1568
AE110s7	TGTAAAACGACGGCCAGTAACGGGTACCAATTCTATCCC	1448	CAGGAAACAGCTATGACCCTAGCACATATCCCAGC	1569
AE110s8	TGTAAAACGACGGCCAGTGATTTTGGGTGGATAGAAGCC	1449	CAGGAAACAGCTATGACCGGTTTACAAACCACTTT	1570
AE110s9	TGTAAAACGACGGCCAGTGAAGGGTGCATGCCTGTAGT	1450	CAGGAAACAGCTATGACCTAAGTGACCTGCCCAAA	1571

Table XII
Sample Description

Race	Cases			Controls			Total
	Angioedema	Angioedema-like	Total	Angioedema	Angioedema-like	Total	
Blacks	11	10	21	32	19	51	72
Caucasians	12	22	34	38	69	107	141
Other	0	1	1	0	1	1	2
Total	23	33	56	70	89	159	215

Table XIII
Candidate Angioedema Susceptibility Genes

Chromosome	Gene	Gene ID
14	Bradykinin B2 Receptor	BDKRB2
19	Tissue Kallikrein	KLK1
X	Aminopeptidase P (Membrane Bound)	XPNPEP2

Table XIV
Association of SNPs of the present invention with Angioedema and/or Angioedema-like Events

Gene ID	SNP ID	Sample or Subgroup	Scores Test	DF	Probability	Estimate Type	A,a[1]	Copies of Rare Allele	Odds Ratio (OR)[2]	OR Lower 95% CL	OR Upper 95% CL	p(a)[3]
BDKRB2	AE104s9	Caucasians	7.01	2	0.0300	Asymptotic	A,T	1	3.41	1.3238	8.7969	0.28
					0.0251	Exact			3.37	1.2261	10.2718	
KLK1	AE107s2	Blacks	7.50	2	0.0062	Asymptotic	C,T	1	5.64	1.4211	22.3807	0.09
					0.0062	Exact			5.64	1.2422	34.7611	
XPNPEP2	AE100s4	Caucasians	13.44	2	0.0009	Exact	C,T	2	14.95	1.9838	+INF	0.28
		Angioedema-like	11.39	2	0.0022	Exact		2	10.82	1.3105	+INF	0.22
		Overall	10.72	2	0.0047	Asymptotic		2	11.11	1.2687	97.2709	0.23

1 Most frequent (common) allele, least frequent (rare) allele.

2 The ratio of the odds of an adverse event (angioedema and/or Angioedema-like) in subjects carrying the specified number of copies of the rare allele, relative to controls matched for nationality, race, gender and starting dose, over the odds of such an adverse event for similarly matched subjects not carrying any copies of the rare allele.

3 Rare allele relative frequency.